

A:Gene: ad 1006
C:Superfamily: Archaeoglobus fulgidus conserved hypothetical protein AP102

Query Match 11.0%; Score 86.5; DB 2; Length 978;
Best Local Similarity 24.4%; Pred. No. 38; Mismatches 41; Indels 19; Gaps 5;

Cy 12 LANTVDEEERHAY REFDLMEKHLKELALFYLLTQTHF...LEK 62
Db 355 LSGSSSIFRRFVCAQCF-----RISFPEVKKFVAFTEPPIVPELESEEV 409

Cy 63 LRLMKALVAMLLIAMDVSVLEPM_RFKLILFLNLMLEKSHILK 121
Db 410 TSLAMKFLVGLLQKFLKFLFQENLQYKKYKHEKVLDELK...LEPELK 465

Cy 122 KEE 124

Db 466 ERE 469

RESULT 7

T29140
hypothetical protein K1104.3 Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15 Nov 1999 #next_change 21-Jan-2000

C:Accession: T29140
R:Paulley, A., Galland, C.
submitted to the EMBL Data Library, July 1996

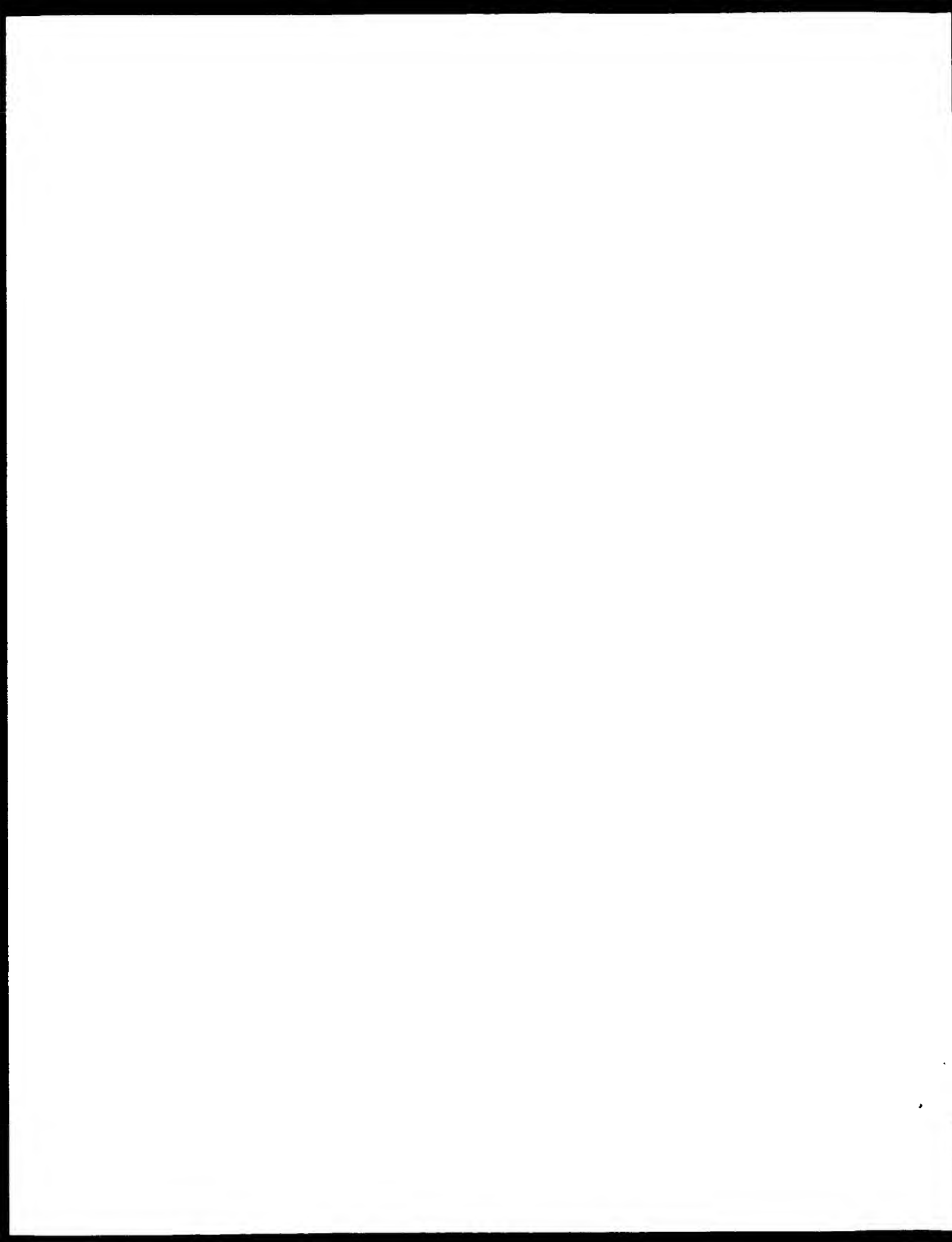
A:Description: The sequence of C. elegans cosmid K1104.
A:Reference number: 22677

A:Accession: T29140
A:Status: preliminary, translated from GE/EMBL/DB

A:Molecule type: DNA
A:Residues: 1-2325 <PAU>

A:Cross-references: EMBL:AB018416; GENBANK:U000024; CDS:K1104.3
A:Experimental source: Strain Bristol N2; clone K1104

C:Genetics:
A:Gene: CDS:K1104.3
A:Map position: 5
A:Introns: 1027, 1122, 1143, 1144, 1145, 1146, 1147, 1148, 1149, 1150, 1151, 1152, 1153, 1154, 1155, 1156, 1157, 1158, 1159, 1160, 1161, 1162, 1163, 1164, 1165, 1166, 1167, 1168, 1169, 1170, 1171, 1172, 1173, 1174, 1175, 1176, 1177, 1178, 1179, 1180, 1181, 1182, 1183, 1184, 1185, 1186, 1187, 1188, 1189, 1190, 1191, 1192, 1193, 1194, 1195, 1196, 1197, 1198, 1199, 1200, 1201, 1202, 1203, 1204, 1205, 1206, 1207, 1208, 1209, 1210, 1211, 1212, 1213, 1214, 1215, 1216, 1217, 1218, 1219, 1220, 1221, 1222, 1223, 1224, 1225, 1226, 1227, 1228, 1229, 1230, 1231, 1232, 1233, 1234, 1235, 1236, 1237, 1238, 1239, 1240, 1241, 1242, 1243, 1244, 1245, 1246, 1247, 1248, 1249, 1250, 1251, 1252, 1253, 1254, 1255, 1256, 1257, 1258, 1259, 1260, 1261, 1262, 1263, 1264, 1265, 1266, 1267, 1268, 1269, 1270, 1271, 1272, 1273, 1274, 1275, 1276, 1277, 1278, 1279, 1280, 1281, 1282, 1283, 1284, 1285, 1286, 1287, 1288, 1289, 1290, 1291, 1292, 1293, 1294, 1295, 1296, 1297, 1298, 1299, 1300, 1301, 1302, 1303, 1304, 1305, 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GenCore version 5.1.4 p5 4578
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CM protein protein search, using sw model

Run on: March 11, 2003, 15:23:44 ; Search time 16.7759 seconds
(without alignments)
326.353 Million cell updates/sec

Title: US-09-877-160-1

Perfect score: 661

Sequence: 1 MFTIAPFVATLAVMTVSGE.....GDLPRDLKKEARVYEV 132

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum hit seq length: 200000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_401*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	652	99.3	132	1	ALL5_DERPT
2	275.5	41.6	134	1	ALL5_DERPT
3	186	29.1	122	1	ALL5_DERPT
4	96	14.5	886	1	RASO_SULAC
5	86.5	13.0	978	1	RASO_SULAC
6	85.5	12.5	254	1	FMN_DROME
7	85.5	12.9	565	1	RECIN_BACHD
8	84	12.7	1433	1	REST_CHICK
9	81.5	12.5	503	1	UVRC_BORBU
10	83	12.5	597	1	YHS_YEAST
11	83	12.5	2245	1	MYSG_DICDI
12	82.5	12.4	727	1	MPPI_ARATH
13	82.5	12.4	878	1	SYA_THETN
14	82.5	12.4	2336	1	YGGI_HUMAN
15	81.5	12.3	1978	1	MYHB_CHICK
16	81	12.2	1072	1	CARB_THETN
17	80.5	12.1	144	1	Y647_APOF1
18	80	12.1	784	1	LCN_ECOLI
19	80	12.1	879	1	RA50_SULTO
20	80	12.1	886	1	RA50_APCFU
21	79	11.9	166	1	YB38_MYCPN
22	79	11.9	559	1	YB37_WHEAT
23	79	11.9	691	1	TCPI_BACSU
24	79	11.9	1972	1	MYHB_HUMAN
25	78.5	11.8	419	1	NEMO_HUMAN
26	78.5	11.8	436	1	EP45_XENLA
27	78.5	11.8	1875	1	MLP1_YEAST
28	78.5	11.8	2869	1	BBP1_PLAUV
29	78	11.8	284	1	TPMW_ANISI
30	78	11.8	448	1	TRME_AQUAE
31	77.5	11.7	578	1	MOEH_DROME
32	77.5	11.7	1055	1	TIRH_HABIN
33	77.5	11.7	1217	1	FLIN_CABEL

34	77	11.6	845	1	SCD1_MESAU
35	77	11.6	914	1	SYA_PYRAB
36	77	11.6	1732	1	UCO1_YEAST
37	77	11.6	1972	1	MYHB_RABIT
38	76.5	11.5	482	1	RASO_PYRFE
39	76.5	11.5	1427	1	REST_HUMAN
40	76	11.5	132	1	KTHY_CAMEL
41	76	11.5	284	1	TPMW_TRICO
42	76	11.5	84	1	RASO_SULTO
43	76	11.5	1163	1	SBAC_GLOAB
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ALIGNMENTS

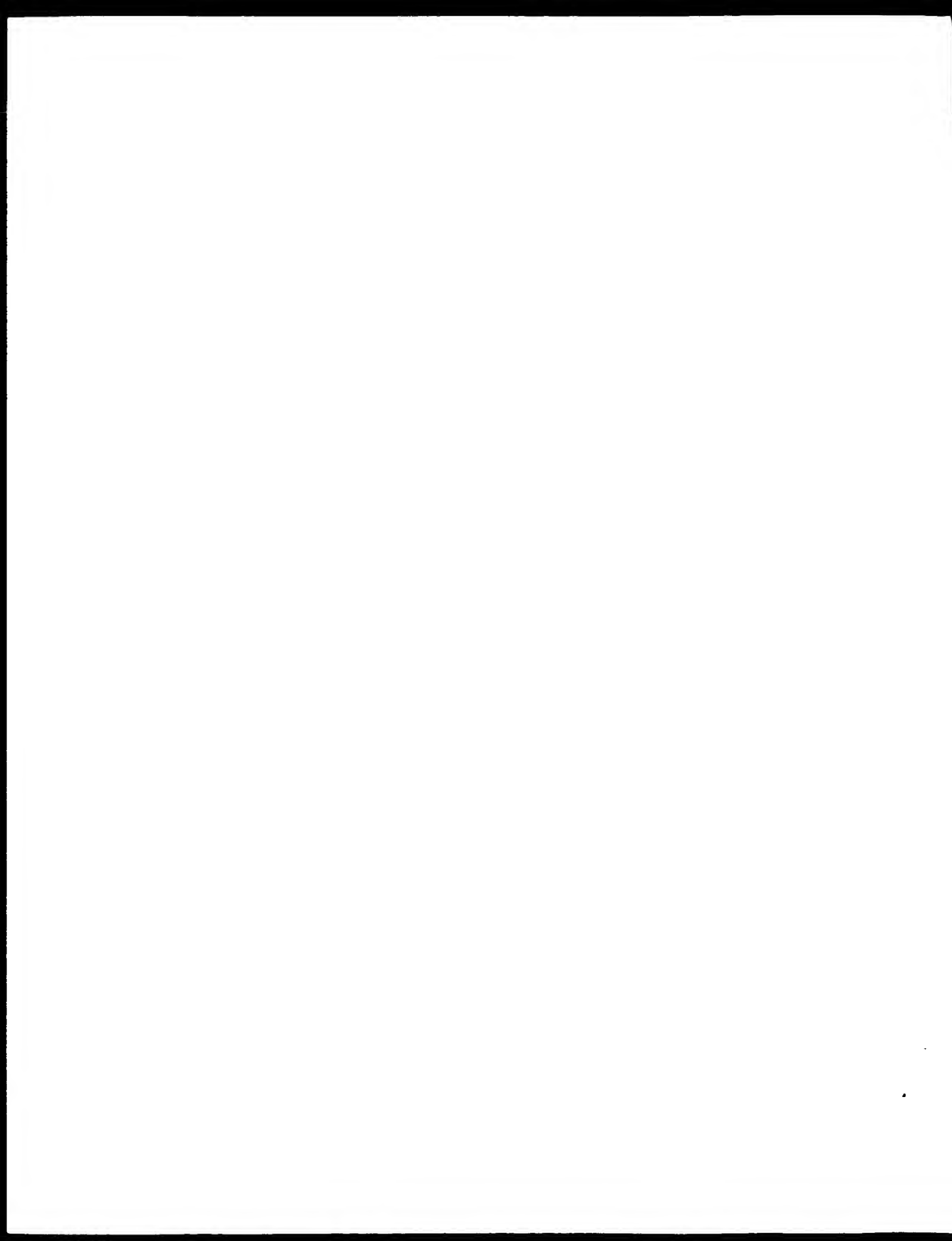
RESULT 1
ALL5_DERPT STANDARD; PRT; 132 AA.
AC P14004;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Mite allergen Der p 5 (Der p V) (Ige-binding allergen).
GN DERP5.
OC Dermatophagoides pteronyssinus (House dust mite).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Acariformes; Sarcoptiformes; Astigmata; Analagida; Pyroglyphidae;
OC Dermatophagoides.
OX NCBI_TaxID=6956;
XX SEQUENCE FROM N.A.
XX MEDLINE=9536459, PubMed=7738547;
PA Lin X.L. Haeh K.H., Thomas W.R., Chiari B.L., Chua X.Y.;
BT "Characterization of Der p V allergen, cDNA analysis, and Ige-mediated
BT reactivity to the recombinant protein.";
EL J. Allergy Clin. Immunol. 94:989 996(1994).
[2]
SEQUENCE FROM N.A.
RX MEDLINE=90010801, PubMed=2794865;
PA Torrey P.P., Johnson M.C., Poche A.L., Cohen G.S., Baldo B.A.;
BT "Cloning and sequencing of a cDNA expressing a secreted mouse dust
BT mite protein that binds human IgE and corresponds to an important low
BT molecular weight allergen.";
KL J. Exp. Med. 173:1457 1462(1990).
[3]
REVISION TO 132.
PA Cobon G.S.;
EL Submit: 24 (FEB 1993) to the EMBL/Genbank/Trill databases.
CC -1- SIMILARITY: BELONGS TO THE MITE GROUP 5 ALLEPSEN FAMILY.
CC This SWISS PROT entry is copyright. It is produced through a collaboration
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DR EMBL; S76337; AAB32841.1;
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DR PIR; S06734; S06734.
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Cv 1 MFTIAPFVATLAVMTVSGE.....GDLPRDLKKEARVYEV 132


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DR InterPro; IPR004009; Myosin N.
DR InterPro; IPR002928; Myosin tail.
DR InterPro; IPR002017; Spectrin.
DR InterPro; IPR001609; myosin_head.
DR Pfam; PF00063; myosin_head; 1.
DR Pfam; PF00612; IQ; 1.
DR Pfam; PF01576; Myosin_tail; 1.
DR Pfam; PF02716; Myosin_N; 1.
DR PRINTS; PR00193; MYOSINHEAVY.
DR ProDom; PD000355; myosin_head; 1.
DR SMART; SM00015; IQ; 1.
DR SMART; SM00242; MYSC; 1.
DR PROSITE; PS00096; IQ; 1.
KW Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding;
KW ATP-binding; Methylation; Alkylation; Calmodulin-binding;
KW Multigene family; 3D-structure.
FT INIT MET 0 0 MYOSIN HEAD-LIKE.
FT DOMAIN 1 790 IQ.
FT DOMAIN 791 820 IQ.
FT DOMAIN 849 1978 RODLIKE TAIL (S2 AND IMM DOMAINS).
FT DOMAIN 849 1578 COILED COIL (POTENTIAL).
FT NP BIND 176 183 ATP.
FT DOMAIN 666 688 ACTIN-BINDING.
FT DOMAIN 767 781 ACTIN-BINDING.
FT MOD_RES 1 1 BLOCKED.
FT MOD_RES 127 127 METHYLATION (TR1) (POTENTIAL).
FT MOD_RES 706 706 ALKYLATION (SH-1).
FT MOD_RES 716 716 ALKYLATION (SH-2).
FT CONFLICT 127 127 MISSING (IN REF. 3).
FT CONFLICT 204 215 KUISITQSPFS->RTASLKVHLFP (IN REF. 1).
SQ SEQUENCE 1978 AA; 43865 MW; 57665956C77C93 ERD54,
Query March 12, 2003; Score 81.5; DB 1; Length 1978;
Best Local Similarity 27.28; Pred. No. 77;
Matches 34; Conservative 27; Mismatches 47; Indels 17; Gaps 7;
Q1 14 LAMININ-RELATED PROTEIN [HUMAN] FFLMPPHFLPFLFPLAFYLLGGINHRRRT.....YE 66
DB 1371 ISTUQLSDSFWVQ-PET-ATVETWEEGHPHQPETPSLTC FEYAAQVYKLEK 1425
QY 67 MEDIVAFPMQTITAMTQVQVIFPIWPPV TMLPEVYMLEMPPKQLLEPQLKYE 103
DB 1425 LAMP-RELATED PROTEIN [HUMAN] FFLMPPHFLPFLFPLAFYLLGGINHRRRT.....YE 66
QY 134 EARVK 128
DB 1482 EAREK 1486

```

Search completed: March 12, 2003, 08:52:03
 Job time : 20.775 secs



GenCore version 5.1.4 p5 4578
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CM protein - protein search, using sw model

Run on: March 11, 2003, 16:11:59 : Search time 33.3331 Seconds
(without alignments)
527,708 Million cell updates/sec

Title: US-09-877-160-1
Perfect score: 63
Sequence: 1 M2E1AAPPVMAAWVSGR QP1PPTFFPFFPFFPFFV IV

Scoring table: BLOSUM62

Gapop 10.0, Gapext 5

Searched: 90470 seqs, 1305622 residues

Total number of hits satisfying chosen parameters 90470

Minimum DB seq length: 0

Maximum Match 100%

Listing first 45 summaries

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database

A Geneseq 161002 *

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2	/SID22/gcgdata/geneseq/geneseq-emb1/AA1981.DAT *
3	/SID22/gcgdata/geneseq/geneseq-emb1/AA1982.DAT *
4	/SID22/gcgdata/geneseq/geneseq-emb1/AA1983.DAT *
5	/SID22/gcgdata/geneseq/geneseq-emb1/AA1984.DAT *
6	/SID22/gcgdata/geneseq/geneseq-emb1/AA1985.DAT *
7	/SID22/gcgdata/geneseq/geneseq-emb1/AA1986.DAT *
8	/SID22/gcgdata/geneseq/geneseq-emb1/AA1987.DAT *
9	/SID22/gcgdata/geneseq/geneseq-emb1/AA1988.DAT *
10	/SID22/gcgdata/geneseq/geneseq-emb1/AA1989.DAT *
11	/SID22/gcgdata/geneseq/geneseq-emb1/AA1990.DAT *
12	/SID22/gcgdata/geneseq/geneseq-emb1/AA1991.DAT *
13	/SID22/gcgdata/geneseq/geneseq-emb1/AA1992.DAT *
14	/SID22/gcgdata/geneseq/geneseq-emb1/AA1993.DAT *
15	/SID22/gcgdata/geneseq/geneseq-emb1/AA1994.DAT *
16	/SID22/gcgdata/geneseq/geneseq-emb1/AA1995.DAT *
17	/SID22/gcgdata/geneseq/geneseq-emb1/AA1996.DAT *
18	/SID22/gcgdata/geneseq/geneseq-emb1/AA1997.DAT *
19	/SID22/gcgdata/geneseq/geneseq-emb1/AA1998.DAT *
20	/SID22/gcgdata/geneseq/geneseq-emb1/AA1999.DAT *
21	/SID22/gcgdata/geneseq/geneseq-emb1/AA2000.DAT *
22	/SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT *
23	/SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	652	98.3	132	20	D. pteronysinus a
2	275.5	41.5	134	22	Domestic mite Bt5
3	275.5	41.6	134	23	Blomia tropicalis
4	275.5	41.6	134	25	Blomia tropicalis
5	270.5	40.8	134	22	Domestic mite Bt5
6	270.5	40.8	134	22	Blomia tropicalis
7	264	33.9	127	22	Domestic mite Bt5
8	264	33.8	127	23	Blomia tropicalis
9	263	39.7	117	22	Colombian mite Bt5
10	263	39.7	117	23	Blomia tropicalis

11	263	39.7	117	23	Blomia tropicalis
12	261	39.4	117	22	Domestic mite Bt5
13	261	39.4	117	22	Domestic mite Bt5
14	261	39.4	117	22	Domestic mite Bt5
15	261	39.4	117	23	Blomia tropicalis
16	261	39.4	117	23	Blomia tropicalis
17	255	38.5	117	22	Colombian mite Bt5
18	255	38.5	117	22	Blomia tropicalis
19	255	38.5	117	23	Blomia tropicalis
20	255	38.5	117	23	Blomia tropicalis
21	178	26.8	84	22	Domestic mite Bt5
22	178	26.8	84	22	Blomia tropicalis
23	169	15.1	782	23	Blomia tropicalis
24	97	14.0	657	17	Blomia tropicalis
25	95.5	14.4	536	23	Blomia tropicalis
26	95.5	14.4	536	23	Blomia tropicalis
27	87	13.1	536	23	Blomia tropicalis
28	87	13.1	536	23	Blomia tropicalis
29	87	13.1	536	23	Blomia tropicalis
30	86	13.0	536	23	Blomia tropicalis
31	85	12.9	536	23	Blomia tropicalis
32	85	12.9	536	23	Blomia tropicalis
33	84.5	12.7	536	23	Blomia tropicalis
34	84.5	12.7	536	23	Blomia tropicalis
35	84	12.7	536	23	Blomia tropicalis
36	82.5	12.4	623	23	Blomia tropicalis
37	82.5	12.4	623	23	Blomia tropicalis
38	81	12.2	1558	21	Blomia tropicalis
39	81	12.2	1558	21	Blomia tropicalis
40	81	12.2	1558	21	Blomia tropicalis
41	81	12.2	1558	21	Blomia tropicalis
42	80	12.1	1456	22	Blomia tropicalis
43	80	12.1	1456	22	Blomia tropicalis
44	79.5	12.0	569	22	Blomia tropicalis
45	73	11.9	816	16	Blomia tropicalis

ALIGNMENTS

RESULT 1

AAV25584

ID AAV25584 standard, protein, 132 AA.

AC AAV25584

XX AAV25584

XX AAV25584

XX AAV25584

XX AAV25584

XX AAV25584

XX AAV25584

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XX AAV25584

XX AAV25584

Major histocompatibility complex, class II, beta chain, human;
allergen, grass, tree, weed, pollen, fungi, mould, insect, sting;
chirididae, spider, mite, housefly, fruit fly, cheet, blow fly, housefly;
screw worm fly; grain weevil; silkworm; bee moth; larvae; mealworm; cat;
blackhead; beetle; dog; horse; cow; pig; sheep; rabbit; rat; guinea pig;
mice; gerbil; vaccine; treatment; prevention; hyperimmunity;
Dermatophagoides pteronysinus;
WO9934826-A1;
15-JUL-1999;
11-JAN-1999; aa00-pp000000;
21-SEP-1998; 98GB-0020474;
09-JAN-1998; 98GB-0000445;
(MCO.) IMPERIAL COLLEGE INNOVATIONS LTD.
Kay AB, Larche M;
WT1, 1999-459055/36.

[illegible]

FR 18-JUL-2000; 2000AU-0008945.
 FR 18-JUL-2000; 2000AU-0008944.
 FR 18-JUL-2000; 2000AU-0008945.
 XX PA (UYSI-) UNIV SINGAPORE NAT.
 XX CHUA KY, Cheong N, Lee BW;

PI Chua KY, Cheong N, Lee BW;
 XX WP1; 2001-10A609/12
 DR N-PSDB; AAD06259.

PT Novel immunogenic protein derived from house mite, Blomia tropicalis
 useful for treating and diagnosing conditions involving induction of
 PT immunoresponse to mite, such as allergic asthma, atopic dermatitis,
 PT rhinitis

XX Example 46; Page 221-222; 220pp; English.

CC The present invention relates to immunogenic proteins, referred as Bt
 CC allergen, is derived from domestic mite, Blomia tropicalis. The specific
 CC Bt allergens of the invention includes Bt1, Bt10, Bt5 and BtA2. The
 CC immunogenic protein is useful for preventing, reducing or ameliorating
 CC Blomia tropicalis hypersensitivity condition such as atopic dermatitis,
 CC immediate hypersensitivity, systemic anaphylaxis, allergic rhinitis or
 CC asthma and for modulating an immune response directed to Bt allergen in
 CC a subject. The Bt allergens are also useful for detecting antibody
 CC directed to all or a part of Bt allergen in a biological sample from a
 CC subject. Antibodies to Bt allergens are also used as therapeutic or
 CC diagnostic agents, to screen Bt immunosensitizers and as antagonists to
 CC inhibit Bt activity under circumstances where temporary hypersensitivity
 CC inhibition is required. The present sequence is Bt5 allergen
 CC polypeptidic amino acid variant.

XX Sequence 127 AA;

Query Match 32.9%; Score 264; DR 23; Length 127;
 Best Local Similarity 42.0%; Pred. No. 3.9e-19;
 Matches 50; Conservative 32; Mismatches 17; Indels 0; Gaps 0;

29 13 AWTGVSQDEHETQNEFDELLMERIHEDTPPELALFVQELQVHFFKFFKFFKFFV 74
 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50
 7 SVLAQEHPTKQKFFKFFKFFKFFKFFKFFKFFKFFKFFKFFKFFKFFKFFKFF 66
 83 AEMETIAWITGVSQDEHETQNEFDELLMERIHEDTPPELALFVQELQVHFFKFFKFFKFFV 131
 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104
 67 RELDVCAMIESAQALPFFKFFKFFKFFKFFKFFKFFKFFKFFKFFKFFKFFKFF 135

RESULT 8
 AAE19278
 ID AAE19278 standard; Protein; 127 AA.

XX AAE19278;

DT 21-MAY-2002 (first entry)

XX Blomia tropicalis Bt5 polypeptidic amino acid variant no. (1)13.

XX Immunogenic polypeptidic Bt5 protein; domestic mite allergen; rhinitis;
 KW hypersensitivity; immune response; allergic asthma; atopic dermatitis;
 KW pharmaceutical composition; antiallergic; antiasthmatic; dermatological;
 KW antiinflammatory; vaccine; gene therapy; mutant; mutein; variant.

XX Blomia tropicalis.

OS Synthetic.

XX W0200206323-A1.

XX 24 JAN 2002.

XX 10-OCT-2000; 2000AU-0008945.

XX 18-JUL-2000; 2000AU-0008945.

XX (UYSI-) UNIV SINGAPORE NAT.
 XX CHUA KY, Cheong N, Lee BW, Liew LN;
 XX WP1; 2002 105803/25.
 DR N-PSDB; AAD30706.

PT Novel immunogenic protein isolated from domestic mite allergen, Blomia
 PT tropicalis, useful for preventing, reducing and ameliorating a
 PT polypeptidic Bt5 hypersensitivity

XX Claim 4, Page 94-95; 101pp; English.

CC The present invention relates to an isolated immunogenic polypeptidic Bt5
 CC protein derived from domestic mite allergen, Blomia tropicalis (Bt). Bt5
 CC is useful for preventing, reducing and ameliorating a polypeptidic Bt5
 CC hypersensitivity. Bt5 is used as vaccine and for modulating an immune
 CC response. Bt5 is useful for detecting antibody directed to all or part of
 CC polypeptidic Bt5 in a biological sample, from a subject, by contacting the
 CC biological sample with Bt5, its derivative, homologue, analogue, mimetic
 CC or chemical equivalent, to form an antibody-protein complex and detecting
 CC the complex. Bt5 is useful for the prophylactic treatment of an allergic
 CC condition (including allergic asthma, atopic dermatitis and/or rhinitis)
 CC in an individual, e.g. human or animal, by administering Bt5 (preferably
 CC in the form of an emulsion) comprising a normal saline or liposome as
 CC pharmaceutical composition comprising a normal saline or liposome as
 CC carrier). Its derivative or homologue, where the airway hyper reactivity or
 CC airway inflammation is prevented. Bt5 gene is useful in gene therapy. The
 CC present sequence is Blomia tropicalis Bt5 polypeptidic amino acid variant.

XX Sequence 127 AA;

Query Match 39.9%; Score 264; DR 23; Length 127;
 Best Local Similarity 42.0%; Pred. No. 3.9e-19;
 Matches 50; Conservative 32; Mismatches 17; Indels 0; Gaps 0;

29 13 AWTGVSQDEHETQNEFDELLMERIHEDTPPELALFVQELQVHFFKFFKFFKFFV 12
 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50
 7 SVLAQEHPTKQKFFKFFKFFKFFKFFKFFKFFKFFKFFKFFKFFKFFKFFKFF 66
 83 AEMETIAWITGVSQDEHETQNEFDELLMERIHEDTPPELALFVQELQVHFFKFFKFFKFFV 131
 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104
 67 RELDVCAMIESAQALPFFKFFKFFKFFKFFKFFKFFKFFKFFKFFKFFKFFKFF 135

RESULT 9
 AAE02251
 ID AAE02251 standard; Protein; 117 AA.

XX AAE02251;

DT 31-JUL-2001 (first entry)

XX Colombian mite Bt5 polypeptidic amino acid sequence no: 5.

XX Mite; immunogenic protein, Bt allergen, therapy, atopic dermatitis;
 KW immediate hypersensitivity, systemic anaphylaxis, allergic rhinitis;
 KW asthma; antiallergic; antiinflammatory; immunosuppressive.

XX Blomia tropicalis.

XX Key Location/Qualifiers

FT Misc-difference 33

FT /note= "Encoded by TTG"

FT Misc-difference 34

FT /note= "Encoded by ATT"

XX W0200130817-A1.

XX 03 MAY 2001.

XX 10-OCT-2000; 2000AU-0008945.




```

Query Match      12.0%; Score 79.5; DB 19; Length 209;
Best Local Similarity 28.3%; Pred. No. 1.4;
Matches 19; Conservative 24; Mismatches 46; Indels 29; Gaps 9;

QY 1 MKF--IIAFVATIAVMIVSCEKKEH--QVNEPFGVLLMPPKHEIIFPSELALFVLDECI 55
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MPEETITAVVAGSVLGGSTTIFRIVAKFVY 51
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 17 MHFEETTEHMLIAEM:III IAMISVPSVPIPMPEELDIFIVNLEMLKSS 112
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 52 AEIDGKFFPTFD VNCVTAVPGRVAVTIIIPNATRIPE... PEKEE DAIKES- 101
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 114 DILKDLKKFAKAVNIE 131
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 102 -EQDFFKAKSHVDNID 116
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 6
US 09-927 597-2
; Sequence 2, Application US/09-927557
; Publication No. US2003032018A1
; GENERAL INFORMATION:
; APPLICANT: Malik, Fady
; APPLICANT: Beraud, Christophe
; APPLICANT: Freedman, Richard
; APPLICANT: Craven, Andrew
; APPLICANT: Sakowitz, Poman
; APPLICANT: Hartman, James
; TITLE OF INVENTION: Human smooth muscle myosin heavy chain
; FILE REFERENCE: CYTOP018
; CURRENT APPLICATION NUMBER: US/09/927,597
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1945
; TYPE: PRT
; ORGANISM: Human
; US 09-927-597 2

Query Match      11.9%; Score 79; DB 9; Length 1945;
Best Local Similarity 25.8%; Pred. No. 2;
Matches 33; Conservative 28; Mismatches 47; Indels 20; Gaps 7;

QY 7 VALLAVTSSCEKKEH--QVNEPFGVLLMPPKHEIIFPSELALFVLDECI 64
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1373 ISTERIQLSCSFFFLQPEA...TVFAIFPFFPFEIEHLT...VEEYAAAYDE 1414
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 65 -FEMKQIVAPMTIIAMISVPSVLLPL--MPPF--DIIFFQVNLKEMKPS--DIIFFPML 140
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1425 LEFTNPGALFGLQVVLGKNG--QVNVN--PFAV--PFAV--PFAV--PFAV--PFAV 1490
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 121 KKEARVK 128
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1481 AEAEAREK 1489
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 7
US 09-927-597 4
; Sequence 4, Application US/09-927597
; Publication No. US/09-927597
; GENERAL INFORMATION:
; APPLICANT: Malik, Fady
; APPLICANT: Beraud, Christophe
; APPLICANT: Freedman, Richard
; APPLICANT: Craven, Andrew
; APPLICANT: Sakowitz, Poman
; APPLICANT: Hartman, James
; TITLE OF INVENTION: Human smooth muscle myosin heavy chain
; FILE REFERENCE: CYTOP018
; CURRENT APPLICATION NUMBER: US/09/927,597
; CURRENT FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 17

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1979
; TYPE: PRT
; ORGANISM: Human
; US 09-927-597-4

Query Match      11.9%; Score 79; DB 9; Length 1979;
Best Local Similarity 25.8%; Pred. No. 2;
Matches 33; Conservative 28; Mismatches 47; Indels 20; Gaps 7;

QY 3 VALLAVTSSCEKKEH--QVNEPFGVLLMPPKHEIIFPSELALFVLDECI 64
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1373 ISTERIQLSCSFFFLQPEA...TVFAIFPFFPFEIEHLT...VEEYAAAYDE 1424
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 65 -FEMKQIVAPMTIIAMISVPSVLLPL--MPPF--DIIFFQVNLKEMKPS--DIIFFPML 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1425 LEFTNPGALFGLQVVLGKNG--QVNVN--PFAV--PFAV--PFAV--PFAV--PFAV 1490
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 121 KKEARVK 129
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1481 AEAEAREK 1489
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 8
US 09-863-049A-2
; Sequence 2, Application US/09-863049A
; Publication No. US20030037055A1
; GENERAL INFORMATION:
; APPLICANT: Kenrick, Sue J.
; APPLICANT: Nelson, David L.
; APPLICANT: Aradhya, Swaroop
; APPLICANT: D'Urso, Michele
; APPLICANT: Wofford, Hayley
; APPLICANT: Munnich, Arnold
; APPLICANT: Smahi, Asmaa
; APPLICANT: Israel, Alain
; APPLICANT: Foustka, Annemarie
; APPLICANT: Lewis, Richard A
; APPLICANT: Levy, Moise
; APPLICANT: Heiss, Nina
; TITLE OF INVENTION: Diagnosis and Treatment of Medical Conditions Associated with Def
; FILE REFERENCE: HO-P019610U1
; CURRENT APPLICATION NUMBER: US/09-863,049A
; CURRENT FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/206,223
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 419
; TYPE: PRT
; ORGANISM: human
; US 09-863-049A-2

Query Match      11.8%; Score 78.5; DB 9; Length 419;
Best Local Similarity 24.6%; Pred. No. 4.2;
Matches 31; Conservative 27; Mismatches 49; Indels 19; Gaps 4;

QY 17 TVSEFQFHCYCNFFFLMPPKHEIIFPSELALFVLDECI 70
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 148 EVVSEFEP NM.....PFAV--PFAV--PFAV--PFAV--PFAV--PFAV--PFAV 400
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 71 IVAEMDTIIAMISVPSVLLPL--MPPF--DIIFFQVNLKEMKPS--DIIFFPML 126
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3-1 PFAV--PFAV--PFAV--PFAV--PFAV--PFAV--PFAV--PFAV--PFAV--PFAV 157
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 127 VNIEV 132
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 359 KRHEV 363
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```



```

CORRESPONDENCE ADDRESS
ADDRESSER: Harness, Dickey & Pierce, P.L.C.
STREET: P.O. Box 828
CITY: Bloomfield Hills
STATE: MI
COUNTRY: USA
ZIP: 48303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/533,306A
FILING DATE: September 25, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, DeAnn F.
REGISTRATION NUMBER: 36483
REFERENCE/DOCKET NUMBER: 0115-009690CB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (910) 641-1600
TELEFAX: (910) 641-0270
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 816 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-533-306A-6

```

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Query Match          11.9%; Score 79; DB 2; Length 916;
Best Local Similarity 25.8%; Pred No. 2.3;
Matches 33; Conservative 29; Mismatches 47; Indels 20; Gaps 7;

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QY 9 VATTAVMTGSGDPEHYVNEPFLMEHETHEIKYDELALFYLCQINHEKPT----64
DB 244 IETNLSISSTPTVLEA2.....AVMAIEFFVFFVEIEHETL VFFMAAVYF 355
C 17 VENTATVETVETVIANVNTVLEL-NVY-LLIIEVTEHLEMLVFFVGLLELL 11
DB 296 IETNLSISSTPTVLEA2.....AVMAIEFFVFFVEIEHETL VFFMAAVYF 355
QY 121 KKEAPVK 128
DB 352 ASAPAPVK 359

```

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RESULT 3
US-08-742-923A-6
Sequence 6, Application US/08/42923A
Patent No. 5869611
GENERAL INFORMATION:
APPLICANT: Liu, Pu
APPLICANT: Collins, Francis S.
APPLICANT: Siciliano, Michael J.
APPLICANT: Claxton, David
TITLE OF INVENTION: Markers for Detection of Chromosome 17
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSER: Harness, Dickey & Pierce, P.L.C.
STREET: P.O. Box 828
CITY: Bloomfield Hills
STATE: MI
COUNTRY: USA
ZIP: 48303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

```

```

CORRESPONDENCE ADDRESS
FILING DATE: No. 5869611ember 1, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, DeAnn F.
REGISTRATION NUMBER: 36483
REFERENCE/DOCKET NUMBER: 0115-009690CB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (910) 641-1600
TELEFAX: (910) 641-0270
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 816 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-742-923A-6

```

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Query Match          11.9%; Score 79; DB 2; Length 916;
Best Local Similarity 25.8%; Pred No. 2.3;
Matches 33; Conservative 29; Mismatches 47; Indels 20; Gaps 7;

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QY 9 VATTAVMTGSGDPEHYVNEPFLMEHETHEIKYDELALFYLCQINHEKPT----64
DB 244 IETNLSISSTPTVLEA2.....AVMAIEFFVFFVEIEHETL VFFMAAVYF 355
C 17 VENTATVETVETVIANVNTVLEL-NVY-LLIIEVTEHLEMLVFFVGLLELL 11
DB 296 IETNLSISSTPTVLEA2.....AVMAIEFFVFFVEIEHETL VFFMAAVYF 355
QY 121 KKEAPVK 128
DB 352 ASAPAPVK 359

```

```

RESULT 4
US-533-306A-4
Sequence 4, Application US/08/533306A
Patent No. 5837457
GENERAL INFORMATION:
APPLICANT: Liu, Pu
APPLICANT: Collins, Francis S.
APPLICANT: Siciliano, Michael J.
APPLICANT: Claxton, David
TITLE OF INVENTION: Markers for Detection of Chromosome 16
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSER: Harness, Dickey & Pierce, P.L.C.
STREET: P.O. Box 828
CITY: Bloomfield Hills
STATE: MI
COUNTRY: USA
ZIP: 48303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/533,306A
FILING DATE: September 25, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, DeAnn F.
REGISTRATION NUMBER: 36483
REFERENCE/DOCKET NUMBER: 0115-009690CB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (910) 641-1600
TELEFAX: (910) 641-0270
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 595 amino acids

```


QY 128 KME 131
DB 221 KME 224

RESULT 8

US-09-149-809-24
Sequence 24, Application No. 5449669
Patent No. 5449669
GENERAL INFORMATION:
APPLICANT: METCALFE, Dean D.
APPLICANT: EAC, Fellussetti V.S.
TITLE OF INVENTION: IDENTIFYING EPITOPES OF A MAJOR
HEAT-STABLE CRUSTACEAN ALLERGEN DERIVED FROM SHRIMP
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS DOS
SOFTWARE: Entomella Release #1.3, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/149,809
FILING DATE: 10-NOV-1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,769
REFERENCE/POCKET NUMBER: 40399/183/NIHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5300
TELEX: 904136
INFORMATION FOR SEQ ID NO. 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 295 amino acids
TYPE: amino acid
TOPOLOGY: linear
US 03 149 809 24

Query Match 11.3%; Score 75; DB 1; Length 285;

Best Local Similarity 23.2%, Pct. Id. 1.6,
Matches 29; Conservative 27; Mismatches 41; Indels 29; Gaps 4;

QY 21 KME 131 YCNFQHLMTSHECTYKPLALFVLEGIN... UPPPPPTV 65
DB 159 KME 224 YCNFQHLMTSHECTYKPLALFVLEGIN... UPPPPPTV 215
L 21 KME 131 YCNFQHLMTSHECTYKPLALFVLEGIN... UPPPPPTV 65
L 21 KME 224 YCNFQHLMTSHECTYKPLALFVLEGIN... UPPPPPTV 215

QY 126 KME 130
DB 266 KME 220

RESULT 9

US-09-149-809-24
Sequence 24, Application No. 5449669
Patent No. 5449669
GENERAL INFORMATION:
APPLICANT: METCALFE, Dean D.
APPLICANT: EAC, Fellussetti V.S.
TITLE OF INVENTION: IDENTIFYING EPITOPES OF A MAJOR
HEAT-STABLE CRUSTACEAN ALLERGEN DERIVED FROM SHRIMP
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

TITLE OF INVENTION: AND APPARATUS TO COLLECT SUCH PROTEINS
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Pass P.C.
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/149,822A
FILING DATE: 11-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CONNELL, GARY J.
REGISTRATION NUMBER: 32,820
REFERENCE/POCKET NUMBER: 2618-17-03
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-0700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO. 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 126 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Xaa - any amino acid
LOCATION: 379
US-09-149-822A-70

Query Match 11.3%; Score 75; DB 1; Length 206;
Best Local Similarity 23.2%, Pct. Id. 4.1;
Matches 24; Conservative 22; Mismatches 40; Indels 24; Gaps 7;

QY 20 KME 131 YCNFQHLMTSHECTYKPLALFVLEGIN... UPPPPPTV 65
DB 159 KME 224 YCNFQHLMTSHECTYKPLALFVLEGIN... UPPPPPTV 215
L 21 KME 131 YCNFQHLMTSHECTYKPLALFVLEGIN... UPPPPPTV 65
L 21 KME 224 YCNFQHLMTSHECTYKPLALFVLEGIN... UPPPPPTV 215
QY 126 KME 130 YCNFQHLMTSHECTYKPLALFVLEGIN... UPPPPPTV 65
DB 266 KME 220 YCNFQHLMTSHECTYKPLALFVLEGIN... UPPPPPTV 215

RESULT 10

US-09-005-069-70
Sequence 24, Application No. 5449669
Patent No. 5449669
GENERAL INFORMATION:
APPLICANT: FRANK, GLENN R.
APPLICANT: HUNTER, SHIRLEY WU
TITLE OF INVENTION: NOVEL EPITOPES OF SALIVA PROTEINS
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Pass P.C.
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

TYPE: amino acid
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:

NAME/KEY: K122

LOCATION: 1-496

OTHER INFORMATION: human TIE 2 ligand 2

US-09-740-223A-16

Query Match: 11.11, Score 73.7, IE 4, Length 496

Best Local Similarity: 20.38, Pred. No. 4.9

Matches: 25, Conservative: 26, Mismatches: 37, Indels: 35, Gaps: 3

QV 27 EHHHETVGEALSLVLCQI
DB 155 EHHHETVGEALSLVLCQI
QV 54 EHHHETVGEALSLVLCQI
DB 215 EHHHETVGEALSLVLCQI
QV 122 KEE 124
DB 275 RDE 277

RESULT 13

US-09-709-189-16

Sequence 15, Application US/09709189

Patent No. 6245335

GENERAL INFORMATION:

APPLICANT: Masure, H. Robert

APPLICANT: Masure, H. Robert

APPLICANT: Masure, H. Robert

APPLICANT: Masure, H. Robert

APPLICANT: Masure, H. Robert

APPLICANT: Masure, H. Robert

APPLICANT: Masure, H. Robert

APPLICANT: Masure, H. Robert

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APPLICANT: Masure, H. Robert

APPLICANT: Masure, H. Robert

APPLICANT: Masure, H. Robert

CORRESPONDENCE ADDRESS:

ADDRESSEE: MEETING, HASTEN & GERSHARDT, P.A.

STREET: 11/100 East 44th Street, Suite 103

CITY: Minneapolis

STATE: Minnesota

COUNTRY: USA

ZIP: 55401

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC DOS/MS DOS

SOFTWARE: Patent In Release #10, Version #1.00

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 50/029,444

FILING DATE: 18-FEB-1997

APPLICATION NUMBER: 50/029,444

FILING DATE: 18-FEB-1997

APPLICATION NUMBER: 50/029,444

FILING DATE: 18-FEB-1997

APPLICATION NUMBER: 50/029,444

FILING DATE: 18-FEB-1997

APPLICATION NUMBER: 50/029,444

FILING DATE: 18-FEB-1997

APPLICATION NUMBER: 50/029,444

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APPLICATION NUMBER: 50/029,444

FILING DATE: 18-FEB-1997

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APPLICATION NUMBER: 50/029,444

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APPLICATION NUMBER: 50/029,444

FILING DATE: 18-FEB-1997

APPLICATION NUMBER: 50/029,444

FILING DATE: 18-FEB-1997

APPLICATION NUMBER: 50/029,444

FILING DATE: 18-FEB-1997

APPLICATION NUMBER: 50/029,444

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APPLICATION NUMBER: 50/029,444

FILING DATE: 18-FEB-1997

APPLICATION NUMBER: 50/029,444

FILING DATE: 18-FEB-1997

APPLICATION NUMBER: 50/029,444

FILING DATE: 18-FEB-1997

APPLICATION NUMBER: 50/029,444

FILING DATE: 18-FEB-1997

APPLICATION NUMBER: 50/029,444

FILING DATE: 18-FEB-1997

APPLICATION NUMBER: 50/029,444

FILING DATE: 18-FEB-1997

APPLICATION NUMBER: 50/029,444

FILING DATE: 18-FEB-1997

APPLICATION NUMBER: 50/029,444

FILING DATE: 18-FEB-1997

APPLICATION NUMBER: 50/029,444

FILING DATE: 18-FEB-1997

APPLICATION NUMBER: 50/029,444

FILING DATE: 18-FEB-1997


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: STATE: New Jersey
: COUNTRY: USA
: ZIP: 07601
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-POS/MS-POS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/847,065
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Jackson Esq., David A.
: REGISTRATION NUMBER: 36,742
: REFERENCE/DOCKET NUMBER: 600-1-158
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 201-487-5800
: TELEFAX: 201-343-1684
: INFORMATION FOR SEQ ID NO: 25:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 631 amino acids
: TYPE: amino acid
: STRANDEDNESS: Single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: HYPOTHEetical: NO
: FRAGMENT TYPE: N-terminal
: US-08 847-065-25

```

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Query Match      11.0%; Score 73; DB 4; Length 631;
Best Local Similarity 27.0%; Pred. No. 7.5;
Matches 27; Conservative 12; Mismatched 13; Indels 28; Gaps 3;

QY 14 LMERHEDQ-----IKKGFALAEVLQRIQNHFFSEYKPKWKIVAFMDTIAMIDGVPV 98
DB 7 LDRKHTQNALNKLNSAIKTYLPE-LNVLEKSKDELSPSEIKYKLVDA----- 54

QY 89 LDRLMQPKTDIFECYNIEMFMKFSQDILEPDLKPEEAPVY 128
DB 55 -----AFKKFKDTLKPGEKVAEAKKKVEEAKKY 83

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Search completed: March 12, 2003, 13:27:22
 Job time : 21.1211 secs



Matches	92, Conservative	93, Mismatched	117, Indels	31, Gaps	111,
Qy	21	14TETETNAFNSVATETEECAAFNPELESVTVASNG3	AINHELDLSLDEF	75
Db	45	10LNSNMINKFYNDEKLYEFEEIKFNQVNIETNFKFNNSVPLGLENFADLSNDEF	104	104
Qy	76	KYFF-LLMEAFAFHHFTGELKNAENAVSLINAFAEICLPQMKVTITLPMGGSCG	132	132
Db	105	NEKYVCSLIDATIGSYDERF-INFD1-----VNLPENVDPKKCAVTPVPHGSCG	157	157
Qy	133	WAFSSVAATIAATLNRQSLDAQGLVQCAQ-IGCHGDIIPGIEVQHNGVQVQSY	191	191
Db	169	WAFSAVATVETNIPFCKVWLSERVQVDFPFCGCGVTVVALEYVAGNIGIRSK	217	217
Qy	192	YVAVAREEYEFHPALAEV-ENQVGLNINWNRKEALATHCAIAVLDGLD	240	240
Db	218	YVYAFATETPA-APVLDIPQNTVYVAVINNSDNLAIAP-IVYVYVLEES	271	271
Qy	247	AFKHVGTETTCRGGVGLQNTNANVGVNAGVGVIVNRSWDTNNGVQSY	299	299
Db	292	PLCLFELIEG-FLVYVAVTAVSYFETDFVYVIFPNSWJIAWSEVQ	322	322

Search completed. March 12, 2003, 13:25:49
Job time : 51.8361 secs




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RESULT 3
CIT004
ID Q95X04 PRELIMINARY; PRT; 107 AA.
AC C3X-4.
DT 01-DEC-2001 (TRENBLREL. 19, Created)
DT 01-DEC-2001 (TRENBLREL. 19, last sequence update)
DT 01-MAR-2002 (TRENBLREL. 20, last annotation update)
DE DE Cysteine Proteinase (Prag-pro).
GN CPW3
OS Dermatophagoides farinae (House dust mite).
OC Pityrogastridae; Acari;
OC Acariformes, Sarcoptiformes; Astigmata; Pyroglyphidae;
OC Dermatophagoides.

```

RESULTS

Q9W192 PRELIMINARY; PRT; 445 AA.
 ID Q9W192;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Presence associated tyrosine protease (Fragmen)
 GN Cpl.
 OS Brassica oleracea (Cauliflower).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Eumetazoa; Opisthokonta; Eudicotyledons; Core eudicot; Fabales;
 OC Eurosidia II; Brassicales; Brassicaceae; Brassica
 CY NRI_TaxID=102.
 [1]
 SEQUENCE FROM N.A.
 RA Ceysse S.A., Sinclair B.K., Watson J.M., Pason J.R.,
 RT "Cysteine proteases and their role in stress response during abiotic stimulation
 RT and control during the process of senescence"
 RL Submitted (SEP 2001) to the EMBL/GenBank/CCP databases.
 DR EMBL; AF454956; AAL60578.1;
 DR InterPro; IPR000119; Granulin
 DR InterPro; IPR000664; Peptidase_C1
 DR InterPro; IPR00169; SH3_P1; SH3_P1
 DR Pfam; PF00396; granulin; 1
 DR Pfam; PF00112; Peptidase_C1; 1
 DR PRINTS; PR00705; PAPAIN
 DR ProDom; PD000154; Peptidase_C1; 1
 DR SMART; SM00277; GRAN; 1
 DR PROSITE; PS00640; THIOL_PROTEASE_ASN; UNKNOWN_1
 DR PROSITE; PS00139; THIOL_PROTEASE_CYS; UNKNOWN_1
 DR PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1
 KW Protease.
 FT NDR TER
 EQ SEQUENCE 445 AA; 44414 MW; E804371E45C1A1D9 CPO64;
 Query Match 23.0%, Score 392.5, DP 10, Length 445,
 Best Local Similarity 23.0%, Pval 0.000000,
 Matches 98; Conservative 68; Mismatches 135; Indels 37; Gaps 11;
 QY 3 IVLAIAIAIALSAV--YAPPSVITFEFFYAFNFSYATFEESAAAPLESVYVYVSN 60
 DB 12 VLLASSELEGTATAPENFEVMEERWLENHNYNGDEHPPPELPMNLFPQDH 71
 QY 61 CGAIN-- HLCGCTCTSEFPPELMAFAFPHLPTFDLMATNACCCNGHAPDI 112
 DB 72 NSVPSQSVPLGLTPFACTNTPFPATYLPSS---PMEPTPSVSPSYLHNVCZKLPEV 127
 QY 113 ELRQMTVTPTPMQAGGSSSWAFSSVAATFSAVLAYGNSLSLAPDELVWASLH--GTH 170
 DB 128 LWRATATVTFVGGT--TWALAA;GAV;SH;HPLDELVCELELVCEVSHHHSS 197
 QY 171 QETTRTFEYTHHNVYPSYTFYVAPF--T--SRACRDEGNS--LYPPNRRER 211
 DB 198 QSLMDYAFQFIISNGIITLEDYVYALDNLCTOKNTFVVYVYVYV--PENNLSK 244
 QY 227 EALACTSAIAVIGISIELLAFPH--YGGFTIICRNVYV--NHAVNYVYVNAVYVW 244
 DB 247 KALANQPSVAIEAGGSPFVYKSGVETGTGUALD-----HGVAVAVYGTSEQDYW 299
 QY 285 IVNSMOTNMGNGYGFPAAMI-----DLMMIEYP 315
 DB 306 IIRNSWSNGESNYVLENNISNSKQVAVMASPP 417
 RESULT 6
 ID Q95VA7 PRELIMINARY; PRT; 326 AA.
 AC Q95VA7;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Cathepsin L.
 GN CAT-LIG.

OS Fasciola gigantica.
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
 OC Euhaptorhida; Platyhelminthes; Fasciolidae; Fasciola.
 CY NCBI_TaxID=46835;
 [1]
 SEQUENCE FROM N.A.
 RA Sothos E., Meenan Y., Glans R., Glans C.V., Koje G., Hofmann A.;
 RT "Molecular cloning of cathepsin L encoding genes from Fasciola
 RT gigantica."
 P1 Submitted (SEP 2001) to the EMBL/GenBank/CCP databases.
 DR EMBL; AF193229; AAL23917.1;
 DR InterPro; IPR000663; Peptidase_C1
 DR InterPro; IPR00169; SH3_P1; SH3_P1
 DR Pfam; PF00112; Peptidase_C1; 1
 DR ProDom; PD000158; Peptidase_C1; 1
 DR PROSITE; PS00640; THIOL_PROTEASE_ASN; UNKNOWN_1
 DR PROSITE; PS00139; THIOL_PROTEASE_CYS; UNKNOWN_1
 DR PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1
 SEQUENCE 326 AA; 37457 MW; 7C3F44E348E64EE1 CPO64;
 Query Match 23.0%, Score 389.5, DP 5, Length 326;
 Best Local Similarity 23.0%, Pval 0.000000,
 Matches 109; Conservative 56; Mismatches 128; Indels 42; Gaps 15;
 QY 5 LATASLLASAVYARFSSSTFEFFYAFNFSYATFEESAAAPLESVYVYVSN-- 61
 DB 3 LFLITVL LAGAPA SNEELNHEWFFYTFYVYVYVYVYVYVYVYVYVYVYVYV 57
 QY 62 -- GAINHLSVLSLSEFPPEL--MCAFAPHLPTFDLMATNACCCNGHAPDI 110
 DB 58 HLLGLVTVTGLGNGQFTLFEFFYAFNFSYATFEESAAAPLESVYVYVSN-- 110
 QY 111 EIDLQMTVTPTPMQAGGSSSWAFSSVAATFSAVLAYGNSLSLAPDELVWASLH-- 166
 DB 111 SIDRQGVYVTEVNAAGGSSSWAFSSVAATFSAVLAYGNSLSLAPDELVWASLH-- 169
 QY 157 HPHVHTTTPHETLTPHNVYPSYTFYVAPF--T--SRACRDEGNS--LYPPNRRER 211
 DB 170 HPSQSMNENYV 227
 QY 224 EIEEALQJTSALAV--G--PCLMAFFHYSFELFLNDLHNSHNAVNYVYVNAVYV 283
 DB 228 ELNQMVFYGFPAVAVATSEF--FWHCEGNS--LYPPNRRER 284
 QY 284 WIVNSMOTNMGNGYGFPAAMI-----DLMMIEYP 315
 DB 285 WISKNSGWSNGESNGYVLENNISNSKQVAVMASPP 326
 RESULT 7
 ID Q24944 PRELIMINARY; PRT; 310 AA.
 AC Q24944;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DE Cathepsin L. (Last annotation update)
 DE Cathepsin L. (Last annotation update)
 DE (CPI)
 GN ECL2
 OS Fasciola hepatica (Liver fluke).
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
 OC Euhaptorhida; Platyhelminthes; Fasciolidae; Fasciola.
 CY NCBI_TaxID=6192;
 [1]
 SEQUENCE FROM N.A.
 RA Heussler V.T., Dobbelaere D.A.E.;
 RT "Cloning of a protease gene family of Fasciola hepatica by the
 RT polymerase chain reaction."
 AL Mol. Biochem. Parasitol. 64:11-23(1994).
 GN CAT-LIG.
 EQ SEQUENCE FROM N.A.
 RX MEDLINE-97418801; PubMed-9274877;

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CQ      296 VPNSWNTMNCNVCYVFAN 105
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DD      287 VFNSTGWTGGCTGYTFAPN 106

RESULT 8
QONGW2 PRELIMINARY, FPF: 106 AA.

ID CNGW2
AC CENGW2;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
PT 01-OCT-2000 (TREMBLrel 15, last sequence update)
PT 01-MAR-2002 (TREMBLrel 20, last annotation update)
DE Cathepsin L.
CN CAT-LID.
CC Pterocarya gigantea.
CCC Eukaryota, Metazoa, Platyhelminthes, Trematoda, Digenea.
OCC Echinostomata, Echinostomata, Furcariidae, Paracriola.
OX NCBI_TaxID=46835;
[1]
RN SEQUENCE FROM N.A.
RP Gram S.V., Grams P., Sabhon P., Vivyanant V., Upatham E.S.;
SFT "Molecular cloning of ciliated metacercariae from Pterocarya gigantea.";
PFI SUBMITTED (FEB-2000) to the EMBL/GenBank/DBJ databases.
PI EMBL: AF239266; AAF44697.1;
DP HSP: P07711; ICUL.
DR MEROPS; COI_033; -.
DR InterPro; IPR000668; Peptidase_C1.
DP InterPro; IPnn0164; SHprot_acsite.
DP Pfam; PF00112; Peptidase_C1; 1.
DR PRINTS; PR00705; PAPAIN.
DR ProDom; PD000159; Peptidase_C1; 1.
DR PROSITE; PS00640; THIOL_PROTEASE_ASN; 1.
DR PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.
DR PROSITE; PS00643; THIOL_PROTEASE_HIS; UNICOWH_1.
SQ Hydrolase; Thiol protease.
SW HYDROLASE 320 AA; 37067 MW; PCZ4954C793PPRNF CP0644;

Query Match 99.9%, Score 190, Dp 5, Length 106;
Best Local Similarity 31.4%; Pred No. 8 Seq.56;
Match 99, Conservative 50, Mismatched 100; Index 99; Gap?

CQ      10 CANCAVAPPCFPRIKFFCAPINPVATTTETEMAFFPEL RPTVVTCVT
       ||||| :|||:|||||
U      9 VIANTGVSVAGCHIKWEWFVTVFVGCATEE PPNIHWNVVHIQHNLEPHCI G 62
       ||||| :|||:|||||

CQ      GC CAHHLDLCLEDFENELMS AEAPSHVTCQRLNAPTNNOSINGADAPIDI PQ 116
       ||||| :|||:|||||
CQ      63 VVTHGLNQGTITVEFFVTVTLTPDSCLNSPGIVAVNPDI-----VPSQLMDW 116

```

[illegible]

DR PFAM: PF00112; Peptidase_C1; 1
 DR PRINTS: PR00765; PAPAIN
 DR PRODOM: PD000159; Peptidase_C1; 1
 DR PROSITE: PS00640; THIOL PROTEASE ASN; 1
 DR PROSITE: PS00640; THIOL PROTEASE CYS; 1
 DR PROSITE: PS00640; THIOL PROTEASE HIS; UNKNOWN_1
 FT NON TER 1 1
 FT CHAIN 92 311 PROCATHEPSIN_L3
 SQ SEQUENCE 311 AA; 35475 MW; 833650CB610445 2084;
 Query Mar 1 22:11; Score 375; DB 5; Length 311;
 Best Local Similarity 29.11; Pred. No. 5.1e-24;
 Matches 91; Conservative 56; Mismatches 142; Indels 36; Gaps 0
 QY 25 TFEVFAFNFYATFFTEFAAPFPLESYVWQKQ GATHESSLSQ 73
 DB 5 SWEFPMYKEY NCAGEHPNNGWNVHIEHSHDFGLVYALGNGQTDPTFE 63
 QY 74 EFNREELMS-ARAFEHETFCLETRACSLNGAPAEIDLRUMKVTFERMGGSSQ 132
 DB 64 EFGATYMENSPVSESCGVSVEAFN... DVPASIMPEYVYVTEVQCCQCC 117
 QY 133 WAFSGVAATESAVL-AYVQGLDLAFQELVCA- SQGHGHTPIPPGIEYIOWNGWV 199
 DB 118 WAFSAGALGEGVWNEFETL-FREGLVLTGTA- WMSGYSWPMWYFLESSELET 176
 QY 199 ESIPIVAVQESQRPENAPFPHISYQIYPPNNKFIPEALQTHSAIVAGIKUDAF 248
 DB 177 AGVYTCVAYEYCE YFEEVAVATSAITVH DENFLMWVJFEHAAVAVLAKSDF 234
 QY 249 RHIGGRTIIGRNGYFPHAVNYVSNAGVDYVWVNSWDYNGWGYGFAAN--- 305
 DB 235 YNVEYTF-ITTFVAVAVAVAVATFETSTWILFSGWVWVBLGWMFAPRZEH 294
 QY 306 -----IDLMMIEEYP 315
 DB 295 MCAIASVASVPMVERPP 311
 RESULT 14
 Q95BJ4 PRELIMINARY; PRT; 331 AA
 AC Q95BJ4
 DT 01-DEC-2001 (TREMBLrel; 19, Created)
 DT 01-DEC-2001 (TREMBLrel; 19, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel; 20, Last annotation update)
 DE Cysteine protease (Fragment).
 OS Blomia tropicalis (Mite)
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
 CC Acariformes; Sarcophormes; Astigmata; Glycyphgidae;
 CC Pabimycodidae; Blomia
 OX NCBI_TaxID=40697;
 RN [1]
 RA MORA C.I., Diaz A.M., Montealegre F., Flores I.;
 RT "Cloning and Expression of Blot 1, a Cysteine Protease Gene 1
 PT Allergen from the Domestic Dust Mite Blomia tropicalis.";
 RC Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases
 DR FMRJ; AF277940; AAY58415.1;
 DR InterPro; IPR000658; Peptidase_C1
 DR Pfam; PF00112; Peptidase_C1
 DR ProDom; PD000159; SHprot acsite.
 DR PROSITE; PS00640; Peptidase_C1; 1
 DR PROSITE; PS00640; THIOL PROTEASE ASN; 1
 DR PROSITE; PS00640; THIOL PROTEASE CYS; 1
 DR PROSITE; PS00640; THIOL PROTEASE HIS; UNKNOWN_1
 KW Protease
 FT NON TER 1 1
 SQ SEQUENCE 331 AA; 36156 MW; 202B45E5E5B2900 3874;
 Query Mar 1 22:11; Score 374; DB 5; Length 331;
 Best Local Similarity 38.51; Pred. No. 5.1e-24;
 Matches 92; Conservative 57; Mismatches 95; Indels 36; Gaps 0

27 109 FAEILLEQMEVTLRPMJRENSWALS KVAETLAVLAVENSGELAAEGLVLAAG-- 166
 DB 2 PANFWQWETHVNLKLENGQWASSWAFANNAVTLVAIDPHNLSSELELLCTHLY 61
 QY 167 ... HAWSTTFEFGSEYTHHRYVLELFFVAREGLDERRNAJ FASGIMLW 217
 DB 62 EFTYCHGSCSEMSFAFYWQVQLQEESEFFEMDNG--SANARFSLPVVSYNLR 120
 QY 121 YFNVNREKALADTHSALAVLIDLELVA FRYVQRTILREMYLPHV HAYVING 274
 DB 121 YPAGTGFQANJ-WMS- FVVYIHTEAHFHL FELLPRAGHDAALHAYVVS 175
 QY 275 YGNAGGVVWVHESWDYWZERYGYVFAANIDLMMIEEYP 315
 DB 176 KSTQASIDYVWKTGWTGQWAGVYVESHWSLGINHJ 216
 RESULT 15
 Q9NGW4 PRELIMINARY; PRT; 336 AA
 AC Q9NGW4
 DT 01-OCT-2000 (TREMBLrel; 15, Created)
 DT 01-OCT-2000 (TREMBLrel; 15, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel; 20, Last annotation update)
 DE Cathepsin L
 OS CAT-L1B
 CC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
 CC Echinozoa; Schistosomata; Fasciolidae, Fasciolidae, Fasciola
 OX NCBI_TaxID=46835;
 RN [1]
 RA Gims S.V., Grass R., Schlon P., Vajant V., Zatlakar E.;
 RT "Molecular Cloning of expressed antigens from Fasciola gigantica";
 BL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases
 DR EMBL; AF239284; AAF44675.1;
 DR HSP; P07711; ICUL
 DR MEOP; C01.033;
 DR InterPro; IPR00668; Peptidase_C1
 DR InterPro; IPR00169; SHprot acsite.
 DR Pfam; PF00112; Peptidase_C1; 1
 DR PROSITE; PS00640; Peptidase_C1; 1
 DR PROSITE; PS00640; THIOL PROTEASE ASN; 1
 DR PROSITE; PS00640; THIOL PROTEASE CYS; 1
 DR PROSITE; PS00640; THIOL PROTEASE HIS; 1
 KW Hydrolyase; Thiol protease
 FT NON TER 1 1
 SQ SEQUENCE 336 AA; 36779 MW; 45F233DDEAE591C 49064;
 Query Match 22.11; Score 374; DB 5; Length 326;
 Best Local Similarity 29.11; Pred. No. 8.6e-24;
 Matches 99; Conservative 64; Mismatches 125; Indels 52; Gaps 13;
 QY 10 LLASAVVAFSSINTREYVFAFNFYATFFTEFAAPFPLESYVWQKQ 61
 DB 5 VLAVTVVLSNULWFWEMMYNKNYNGAETH EPHWEENVCHIEHNLHPLGL 62
 QY 62 ...GAIHHLGLSLGDFEFL---MSAEAFELHITFELMAINAGSINGNAPAEID 113
 DB 62 VTYDGLNFTMTTEEPYAVYLTMPFASLISH---GIPVEAN---NNAVPERID 113
 QY 114 LKMTIVITFPMZQWQWMSWQATEALANFPLSLALFPLVLA--LHCH 170
 DB 114 WEECVTEVINGQWGSWALSSTIMEGATNRELSGLTEGQWVLAHAKGLAM 170
 QY 171 GDTIPRGIEYIOWNGYVSESYVASESCFFPMAFPG FSNVCCVYVNFIRE 227
 DB 171 GDMENATEYTFPLFTFQYDTNPFQV FVLEVAVVTVYVTVVLEHLEN 241
 QY 248 ALATHALAVILHIELCA-PEHICSTLLESGHGTNNHAYVAVHRAAGLW 290
 DB 232 LVASBPAAVAV...EVECFMFGQVIGSTFISLFWHAYVAVVAVVAGLW 296

```

QY 266 UNCGWTHWNGNGNGTAA--IDNNIEYP 315
      ||| ||| |||
DB 267 UNCGWIEGRTGRTWVFGNGGACAGNATAP 326

```

Search completed: March 12, 2003, 11:23:34
Job time : 74.1706 secs

GenCore version 5.1.4 p4400
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OM protein - protein search, using sw model

Run on: March 11, 2003, 15:11:59 Search time 80.8027 seconds
(without alignments)
527,709 William cell updates/sec

Title: US-09-877-160-2

Perfect score: 1689
Sequence: 1 METVLAALAIACAVYAP YFAMTOLMMEYVWVL 227

Scoring table: BLOSUM62 Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 11250620 residues

Total number of hits satisfying chosen parameters 908470

Minimum DB seq length: 0

Maximum Match: 08

Post processing: Maximum March 1008

Listing first 45 summaries

Database: A_Genecore_101002.*

1	/SI1522/gdata/geneseq/geneseq-emb1/AA1941.EAT.*	1689	100.0	320	20	AAV25580	D. pteronyssinus
2	/SI1522/gdata/geneseq/geneseq-emb1/AA1941.EAT.*	1689	100.0	320	20	AAV25580	D. pteronyssinus
3	/SI1522/gdata/geneseq/geneseq-emb1/AA1941.EAT.*	1689	100.0	320	20	AAV25580	D. pteronyssinus
4	/SI1522/gdata/geneseq/geneseq-emb1/AA1941.EAT.*	1689	100.0	320	20	AAV25580	D. pteronyssinus
5	/SI1522/gdata/geneseq/geneseq-emb1/AA1941.EAT.*	1689	100.0	320	20	AAV25580	D. pteronyssinus
6	/SI1522/gdata/geneseq/geneseq-emb1/AA1941.EAT.*	1689	100.0	320	20	AAV25580	D. pteronyssinus
7	/SI1522/gdata/geneseq/geneseq-emb1/AA1941.EAT.*	1689	100.0	320	20	AAV25580	D. pteronyssinus
8	/SI1522/gdata/geneseq/geneseq-emb1/AA1941.EAT.*	1689	100.0	320	20	AAV25580	D. pteronyssinus
9	/SI1522/gdata/geneseq/geneseq-emb1/AA1941.EAT.*	1689	100.0	320	20	AAV25580	D. pteronyssinus
10	/SI1522/gdata/geneseq/geneseq-emb1/AA1941.EAT.*	1689	100.0	320	20	AAV25580	D. pteronyssinus
11	/SI1522/gdata/geneseq/geneseq-emb1/AA1941.EAT.*	1689	100.0	320	20	AAV25580	D. pteronyssinus
12	/SI1522/gdata/geneseq/geneseq-emb1/AA1941.EAT.*	1689	100.0	320	20	AAV25580	D. pteronyssinus
13	/SI1522/gdata/geneseq/geneseq-emb1/AA1941.EAT.*	1689	100.0	320	20	AAV25580	D. pteronyssinus
14	/SI1522/gdata/geneseq/geneseq-emb1/AA1941.EAT.*	1689	100.0	320	20	AAV25580	D. pteronyssinus
15	/SI1522/gdata/geneseq/geneseq-emb1/AA1941.EAT.*	1689	100.0	320	20	AAV25580	D. pteronyssinus
16	/SI1522/gdata/geneseq/geneseq-emb1/AA1941.EAT.*	1689	100.0	320	20	AAV25580	D. pteronyssinus
17	/SI1522/gdata/geneseq/geneseq-emb1/AA1941.EAT.*	1689	100.0	320	20	AAV25580	D. pteronyssinus
18	/SI1522/gdata/geneseq/geneseq-emb1/AA1941.EAT.*	1689	100.0	320	20	AAV25580	D. pteronyssinus
19	/SI1522/gdata/geneseq/geneseq-emb1/AA1941.EAT.*	1689	100.0	320	20	AAV25580	D. pteronyssinus
20	/SI1522/gdata/geneseq/geneseq-emb1/AA1941.EAT.*	1689	100.0	320	20	AAV25580	D. pteronyssinus
21	/SI1522/gdata/geneseq/geneseq-emb1/AA1941.EAT.*	1689	100.0	320	20	AAV25580	D. pteronyssinus
22	/SI1522/gdata/geneseq/geneseq-emb1/AA1941.EAT.*	1689	100.0	320	20	AAV25580	D. pteronyssinus
23	/SI1522/gdata/geneseq/geneseq-emb1/AA1941.EAT.*	1689	100.0	320	20	AAV25580	D. pteronyssinus

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	EB	EC	Description
1	1689	100.0	320	20	AAV25580	D. pteronyssinus
2	1689	100.0	320	20	AAV25580	D. pteronyssinus
3	1689	100.0	320	20	AAV25580	D. pteronyssinus
4	1689	100.0	320	20	AAV25580	D. pteronyssinus
5	1679	99.4	320	20	AAV25580	D. pteronyssinus
6	1677	99.3	320	16	AAV25580	D. pteronyssinus
7	1650.5	97.7	316	20	AAV25580	D. pteronyssinus
8	1612	95.4	302	22	AAV25580	D. pteronyssinus
9	1612	95.4	303	22	AAV25580	D. pteronyssinus
10	1608	95.2	302	22	AAV25580	D. pteronyssinus

11	1608	95.2	302	22	AAV25580	Recombinant dust m
12	1608	95.1	343	22	AAV25580	D. pteronyssinus m
13	1604	95.1	362	22	AAV25580	D. pteronyssinus p
14	1582.5	93.7	339	20	AAV25580	D. pteronyssinus m
15	1453.5	86.1	321	22	AAV25580	E. maynei Group 1
16	1433.5	84.9	321	22	AAV25580	Recombinant Derf1
17	1433.5	84.9	321	16	AAV25580	Recombinant Derf1
18	1433.5	84.9	330	16	AAV25580	Recombinant mite a
19	1425.5	84.4	321	13	AAV25580	Der f 1 allergen.
20	1425.5	84.4	321	14	AAV25580	Recombinant Derf1
21	1425.5	84.4	321	15	AAV25580	Protein allergen o
22	1425.5	84.4	321	15	AAV25580	Der f 1. Dermatop
23	1425.5	84.4	321	19	AAV25580	Dermatophagoides D
24	1425.5	84.4	321	22	AAV25580	Recombinant Derf1
25	1425.5	84.4	321	22	AAV25580	Recombinant Derf1
26	1425.5	84.4	321	22	AAV25580	House dust mite al
27	1396.5	82.7	319	20	AAV25580	D. farinae allergen
28	1381.5	81.8	302	22	AAV25580	E. maynei Group 1
29	1368.5	81.0	303	16	AAV25580	Recombinant Derf1
30	1368.5	81.0	303	16	AAV25580	Recombinant Derf1
31	1367.5	81.0	302	22	AAV25580	D. farinae Der f 1
32	1367.5	81.0	304	21	AAV25580	Tick allergen ber
33	1360.5	80.6	303	22	AAV25580	D. farinae Group 1
34	1357.5	80.4	303	22	AAV25580	D. farinae Der f 1
35	1357.5	80.4	303	22	AAV25580	D. farinae Der f 1
36	1354.5	80.2	303	22	AAV25580	D. farinae Der f 1
37	1313	77.7	245	12	AAV25580	Der p 1 allergen.
38	1313	77.7	245	14	AAV25580	Dermatophagoides p
39	1313	77.7	245	15	AAV25580	Protein allergen o
40	1313	77.7	245	15	AAV25580	Der p 1. Dermatop
41	1313	77.7	245	15	AAV25580	Der p 1 allergen.
42	1313	77.7	245	15	AAV25580	Dermatophagoides p
43	1313	77.7	245	22	AAV25580	Recombinant Derf1
44	1313	77.7	245	22	AAV25580	Recombinant Derf1
45	1271.5	75.3	181	12	AAV25580	Recombinant Derf1

ALIGNMENTS

RESULT 1
AAV25580
10 AAV25580 standard; protein; 310 AA.
AC AAV25580;
XX 30-SEP-1999 (first entry)
DE D. pteronyssinus allergen Der p 1 protein fragment.

XX Major histocompatibility complex, class II, desmodiosin; human;
XX allergen. Glass, tree, weed, pollen, food, mold, food, insect, sting;
XX thirividae, spider, mite, housefly, fruit fly, sheep blow fly, housefly;
XX screw worm fly; Grain weevil; silkworm; bee mite; larvae; woolworm; cat;
XX cockroach; beetle; dog; horse; cow; pig; sheep; rabbit; rat; guinea pig;
XX mite; germ; vaccine; treatment; prevention; hypersensitivity.

XX Dermatophagoides pteronyssinus.
XX WO934826-A1.
XX 15-JUL-1999.

XX 11-JAN-1999; 44W-0000000.
XX 21-SEP-1998, 98GB 0000474.
XX 09-JAN-1998, 98GB 0000445.
XX (PMO-1) IMPERIAL COLLEGE INNOVATIONS LTD.
XX Ray AP, Larche M;
XX WI, 1999-459-05/38.

XX D. pteronyssinus Der p 1 protein pDerp1 320.
 XX Mite group 1 protein; methylerophilic yeast; Escherichia coli; allergy;
 KW recombinant mite group 1 protein; allergen; allergic disease;
 KW infectious disease; allergic disease.
 XX Dermatophagoides pteronyssinus.
 OS
 PN W0200129078-A2.
 XX 26 APR 2001.
 XX 12 OCT 2001, 11:17 AM, 1028254.
 XX 15 OCT 1999, 0905-0159841
 XX (HRSK-A) HPSVA CAPP
 XX Host EA, M-Dermatophagoides M1;
 XX N-PSDB; AAH22332.
 XX WPI; 2001-308475/32.
 XX N-PSDB; AAH22332.
 XX Producing recombinant mite Group 1 protein for treating allergies,
 PT involves culturing a methylerophilic yeast microorganism or Escherichia
 PT coli transformed with nucleic acid molecule, and recovering the protein
 PT
 XX
 PS Claim 12; Page 87-88; 154pp; English
 XX The present invention describes a method for the production of a
 CC recombinant mite Group 1 protein (I). The method comprises culturing a
 CC methylerophilic yeast microorganism transformed with a nucleic acid
 CC molecule (II) encoding (i), and recovering (i), or culturing Escherichia
 CC coli transformed with (ii) under conditions in which (i) forms an
 CC inclusion body in E. coli, isolating the inclusion body, and recovering
 CC (i). Also described is a method for detecting mite allergy in an animal
 CC comprising: (a) contacting (i) with a putative IgE-containing substance
 CC to form a complex between (i) and IgE; and (b) determining the presence
 CC of IgE relative with (i) by detecting the complex, where the presence of
 CC reactive IgE is indicative of mite allergy in the animal. (i) is useful
 CC for detecting mite allergy in an animal, or in a composition to reduce
 CC allergic response to a mite Group 1 protein in a mite allergic animal.
 CC (i) is also useful in a composition for treating or preventing allergic,
 CC infectious or other diseases. AAH22332 to AAH2394 and AAH28326 to
 CC AAH98349 represent sequences used in the exemplification of the present
 CC invention
 XX
 XX Sequence 320 AA;
 Query Match 100.0%, Score 1000, EP 17, Length 320,
 Best Local Similarity 100.0%, Pred. No. 26-165;
 Matches 320, Conservative 0, Mismatches 0, Indels 0, Gaps 0;
 QY 1 MKVLATASLALCAVAPRPSSTTTEFFVPAPRPSVATETFEAARFPPFPPVYVSN 60
 DB 1 MKVLATASLALCAVAPRPSSTTTEFFVPAPRPSVATETFEAARFPPFPPVYVSN 60
 QY 61 GGAINHLSDLEDFEPPRFMSAFAERHKTGFLRAETHNACSNINAPAEIDLRMTV 120
 DB 61 GGAINHLSDLEDFEPPRFMSAFAERHKTGFLRAETHNACSNINAPAEIDLRMTV 120
 QY 121 TPIMQGGCGGWSAFSSVATERYAYVNSLCCALDELWQTAQAGYFAPNIPSTAY 160
 DB 121 TPIMQGGCGGWSAFSSVATERYAYVNSLCCALDELWQTAQAGYFAPNIPSTAY 160
 QY 161 TCRNVPVCEKAKKVAQKQVSGTANAPRPSSTTTPPNVNNKILPEALQVHSAIYV 240
 DB 161 TCRNVPVCEKAKKVAQKQVSGTANAPRPSSTTTPPNVNNKILPEALQVHSAIYV 240
 QY 241 QTKLDAEPFLDPRITLTPFLMGEYFNTHAVNIVSYNACVQVYVENSGLNWSLNGY 300
 DB 241 QTKLDAEPFLDPRITLTPFLMGEYFNTHAVNIVSYNACVQVYVENSGLNWSLNGY 300

CE 241 GFELLEALRGLGKLTLLKLENGYQNNHAGVIVGSRAGSGLVWVYKRWLWMLKLTG 300
 QY 301 YEANIDLMMIEBPVYVIL 320
 XX ||||||||||||||||||
 CE 302 YEANIDLMMIEBPVYVIL 320
 XX ||||||||||||||||||
 RESULT 4
 AAY08593
 ID AAY08593 standard; Protein: 320 AA.
 XX AC AAY08593;
 XX 03 AUG 1999 (first entry)
 XX D. pteronyssinus Derp1 allergen mutant G132A protein.
 XX Allergen; Derp1; house dust mite; anti allergic; immunosuppressive;
 KW most cell degranulation; interferon 4 synthesis; allergy specific IgE;
 KW interleukin 4 secretion; allergy; treatment; vaccine; mutant;
 KW Th1 type immune response; Derp1 specific IgG.
 XX
 OS Dermatophagoides pteronyssinus.
 OS Synthetic.
 OS
 PN W020028223-A2.
 XX 27-MAY-1999.
 XX 16-NOV-1998; 9800-EP07521.
 XX 19-NOV-1997, 970B-0024531.
 XX (CMIF) SMITHLINE RESEARCH PLASMA INC.
 XX Bollen A, Bruck C, Jacobs P, Massner M;
 XX WPI, 1999-347471/23.
 XX N-PSDB; AAH24473.
 XX Recombinant mutant Derp1 allergen with reduced enzymatic activity
 XX
 XX Claim 12, Page 39-40, 46pp, English.
 XX This invention describes novel recombinant mutant allergens derived from
 CC the Dermatophagoides pteronyssinus (house dust mite) Derp1 allergen which
 CC have reduced enzymatic activity compared to the wild type allergen and
 CC are anti allergic and immunosuppressive. The allergens induce mast cell
 CC degranulation to stimulate interleukin 4 synthesis and secretion, even
 CC in the absence of allergen specific IgE. The mutant allergens are useful
 CC in manufacture of medicaments for the treatment of allergy. Vaccines
 CC comprising the mutant allergens are useful for treatment and prevention of
 CC allergic responses, particularly to house dust mite. The mutant allergens
 CC increase the Th1 type aspect of immune responses in comparison to those
 CC stimulated by the wild type allergen, leading to the suppression of
 CC allergic potential of the vaccine itself. They also have reduced
 CC allergenicity and are hence more suitable for systemic administration at
 CC high doses. The mutant allergens also induce Derp1 specific IgG which
 CC compete with IgE for the binding of native Derp1.
 XX
 XX Sequence 320 AA;
 Query Match 99.5%, Score 1000, EP 20, Length 320,
 Best Local Similarity 99.5%, Pred. No. 170-164;
 Matches 319, Conservative 0, Mismatches 1, Indels 0, Gaps 0;
 QY 1 MKVLATASLALCAVAPRPSSTTTEFFVPAPRPSVATETFEAARFPPFPPVYVSN 60
 DB 1 MKVLATASLALCAVAPRPSSTTTEFFVPAPRPSVATETFEAARFPPFPPVYVSN 60
 QY 61 GGAINHLSDLEDFEPPRFMSAFAERHKTGFLRAETHNACSNINAPAEIDLRMTV 120
 DB 61 GGAINHLSDLEDFEPPRFMSAFAERHKTGFLRAETHNACSNINAPAEIDLRMTV 120

CC 121 THLENZGSSGMAHSGVAAIESAYLAHNSGSLAEELVLTACNSHSTTTPSTPT 140
 |||||
 DB 121 TPIMQGGCSAWAFSSVAATESAYLAVPNSGLAEDELVTGASRGCHGDTIPRGIEY 180
 |||||
 CY 141 LQNGVWLESYHVAASELSGTFPPHAEHLEKTPDLNAETNACISYNADAFIPISOMSTV 120
 |||||
 DB 141 LQNGVWLESYHVAASELSGTFPPHAEHLEKTPDLNAETNACISYNADAFIPISOMSTV 120
 |||||
 QY 241 LQNGVWLESYHVAASELSGTFPPHAEHLEKTPDLNAETNACISYNADAFIPISOMSTV 120
 |||||
 DB 241 LQNGVWLESYHVAASELSGTFPPHAEHLEKTPDLNAETNACISYNADAFIPISOMSTV 120
 |||||
 QY 301 YFAANIDLMMEIEEYPVVIL 320
 |||||
 DB 301 YFAANIDLMMEIEEYPVVIL 320
 |||||

RESULT 5

AA098595
 ID AA098595 standard; protein; 320 AA.
 XX
 AC AA098595,
 XX
 DT 05-AUG-1999 (first entry)
 XX
 DE D. pteronyssinus Derp1 allergen mutant H268A protein.
 XX
 KW Allergen; Derp1; house dust mite; anti-allergic; immunosuppressive;
 KW mast cell degranulation; interleukin-4 synthesis; allergen-specific IgE;
 KW interleukin-4 secretion; allergy; treatment; vaccine; mutant;
 KW Th1-type immune response; Derp1-specific IgG.
 XX

OS Dermatophagoides pteronyssinus.
 OS Synthetic.

XX WO99259231-A2.

XX 27-MAY-1999.

XX 16-NOV-1998; 98WO-EP07521.

XX 19-NOV-1997; 97GB-0024531.

PA (SWIF) SMITHKLINE BEECHAM BIOLOGICALS

PI Bollen A, Brock C, Jacobs P, Macsaer M;

XX WPI; 1999-347471/29.

XX N PDB; AA02475.

FT Recombinant mutant Derp1 allergen with reduced enzymatic activity;

XX Claim 14; Page 43 44; 46pp; English.

CC This invention describes novel recombinant mutant allergens derived from
 CC the Dermatophagoides pteronyssinus (dust mite) Derp1 allergen which
 CC have reduced enzymatic activity compared to the wild-type allergen and
 CC are anti-allergic and immunosuppressive. The allergens induce mast cell
 CC degranulation to stimulate interleukin-4 synthesis and secretion, even
 CC in the absence of allergen specific IgE. The mutant allergens are useful
 CC in manufacture of medicaments for the treatment of allergy. Vaccines
 CC comprising the mutant allergens are useful for treatment or prevention of
 CC allergic responses, particularly to house dust mite. The mutant allergens
 CC increase the Th1-type aspect of immune responses in comparison to those
 CC stimulated by the wild-type allergen, leading to the suppression of
 CC allergic potential of the vaccinated host. They also have reduced
 CC allergenicity and are hence more suitable for systemic administration at
 CC high doses. The mutant allergens also induce Derp1 specific IgG which
 CC compete with IgE for the binding of native Derp1.

XX Sequence 320 AA;

Query Match 99.48; Score 1679; DE 20; Length 320;
 Post-local similarity 99.81; Posed DE 2 0e-154;
 Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MKIVLAIASLISAVVAPSSITTEEYPAFNZYATFEDEEAAPPPIPPSPVYVARN 40
 |||||
 DB 1 MKIVLAIASLISAVVAPSSITTEEYPAFNZYATFEDEEAAPPPIPPSPVYVARN 40
 |||||
 QY 61 GGAINHLIDLSLDEFFORFELMGAFAEHLKTPDLNAETNACISYNADAFIPISOMSTV 120
 |||||
 DB 61 GGAINHLIDLSLDEFFORFELMGAFAEHLKTPDLNAETNACISYNADAFIPISOMSTV 120
 |||||
 QY 121 TPIPMQGGCSAWAFSSVAATESAYLAVPNSGLAEDELVTGASRGCHGDTIPRGIEY 180
 |||||
 DB 121 TPIPMQGGCSAWAFSSVAATESAYLAVPNSGLAEDELVTGASRGCHGDTIPRGIEY 180
 |||||
 QY 191 LQNGVWLESYHVAASELSGTFPPHAEHLEKTPDLNAETNACISYNADAFIPISOMSTV 120
 |||||
 DB 191 LQNGVWLESYHVAASELSGTFPPHAEHLEKTPDLNAETNACISYNADAFIPISOMSTV 120
 |||||
 QY 301 YFAANIDLMMEIEEYPVVIL 320
 |||||
 DB 301 YFAANIDLMMEIEEYPVVIL 320
 |||||

RESULT 6

AA049920
 ID A049920 standard; Protein; 320 AA.

XX ASP49920;

XX 17-OCT-1994 (first entry)

XX Protein allergen of Der p1.

XX Der p1; House Dust Mite Allergen.

XX Dermatophagoides pteronyssinus.

XX Key Location/Qualifiers

XX Protein 1..322 Der p1 preproenzyme

XX Cleavage-site 2..95

XX /label= Cleavage site

XX /notes= "proenzyme remains"

XX Cleavage-site 25..97

XX /label= cleavage site

XX /note= "cleavage between pro-Der p1 and

XX pre-Der p1"

XX WO9405790-A.

XX 17-MAY-1994.

XX 10-SEP-1993; 93WO-US08518.

XX 10 SEP 1993; 92WO-0045388.

XX (IMMUNO) IMMUNOCYC PHARM CORP.

XX Chua K, Thomas WP;

XX WPI; 1994-181195/10.

XX N-PDB; AA02475.

XX New protein allergens of house dust mite used for diagnosing

XX and treating sensitivity in an individual to house dust mite

XX allergens

Example 1: P17 21. 98pp, English.

AA049020 is a proenzyme Der p1. The amino acid sequence preceding the mature protein sequence contains cleavage sites for the pro- and proenzyme forms, with residues 1-97 corresponding to a partial signal peptide sequence. The mature protein can be used to detect sensitivity in an individual to house dust mite and to reduce the sensitivity of the individual.

Sequence 320 AA;

Query Match 99.1%, Score 1677, DB 15, Length 320,
Best Local Similarity 99.1%, Prob. Max 1.0e-164;
Matches 317; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
1 MEIVLAIASLALSAVAVARPSSTPTFFPPYAPNPSVATPEDESMAPKPLESVVYQSN 60
1 MEIVLAIASLALSAVAVARPSSTPTFFPPYAPNPSVATPEDESMAPKPLESVVYQSN 60
61 GGAINHLSLSLEPPHFMGSAFAFEHLTPTFELMAFTNACSTUNAPAEIDLPMPYTV 120
61 GGAINHLSLSLEPPHFMGSAFAFEHLTPTFELMAFTNACSTUNAPAEIDLPMPYTV 120
121 TPIRMGGGSGSWAFSGVAATESAYLAVENGLMLAFORLWICASLSSPACTIPREIEY 180
121 TPIRMGGGSGSWAFSGVAATESAYLAVENGLMLAFORLWICASLSSPACTIPREIEY 180
181 IOHNVGSGSYYPVAFSGPPPPNAPQFQISNYCQIYPPNPNKIDELACTHSAIAVII 240
181 IOHNVGSGSYYPVAFSGPPPPNAPQFQISNYCQIYPPNPNKIDELACTHSAIAVII 240
241 GIKELDAFRHIGSTIIQPENGYFENHANNIVSTNSMAQSGVWIVRNSWETWJGNG 300
241 GIKELDAFRHIGSTIIQPENGYFENHANNIVSTNSMAQSGVWIVRNSWETWJGNG 300
301 YFAANIDUMMIEEYPYVIL 320
301 YFAANIDUMMIEEYPYVIL 320

RESULT 7

AA0490594

10 AA0490594 standard; Protein, 315 AA.

AA0490594;

0% AUG-1999 (first entry)

D. pteronyssinus Der p1 allergen deletion mutant protein.

Allergen; Der p1; house dust mite; anti-allergic; immunosuppressive;

mast cell degranulation; interleukin-4 synthesis; allergen-specific IgE;

interleukin-4 secretion; allergy; treatment; vaccine; mutant;

This type immune response; Der p1 specific IgG

Dermatophagoides pteronyssinus.

Synthetic.

W09925823-A2.

27-MAY-1999.

16 NOV 1998; 98W0-EP0721

19-NOV 1997; 97GB-0024531.

(SMK) SMITHKLINE BEECHAM BIOLOGICALS.

Bollen A, Bruck C, Jacobs P, Moscaer M;

WPI; 1999-347471/29.

N FDCP; AA0490594.

Recombinant mutant Der p1 allergen with reduced enzymatic activity

Claim 12, Page 41-42, 16pp; English.

This invention describes novel recombinant mutant allergens derived from the dermatophagoides pteronyssinus (dust mite) Der p1 allergen which have reduced enzymatic activity compared to the wild type allergen and are anti allergic and immunosuppressive. The allergens induce mast cell degranulation to stimulate interleukin 4 synthesis and secretion, even in the absence of allergen-specific IgE. The mutant allergens are useful in manufacture of medicaments for the treatment of allergy. Vaccines comprising the mutant allergens are useful for treatment or prevention of allergic responses, particularly to house dust mite. The mutant allergens increase the Th1-type aspect of immune responses in comparison to those stimulated by the wild-type allergen, leading to the suppression of allergic potential of the vaccinated host. They also have reduced allergenicity and are hence more suitable for systemic administration at high doses. The mutant allergens also induce Der p1 specific IgG which compete with IgE for the binding of native Der p1.

Sequence 315 AA;

Query Match 97.7%, Score 1650.5; DB 20; Length 315;
Best Local Similarity 98.4%; Prob. Max 1.0e 161;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 1;
1 MKIVLAIASLALSAVAVARPSSTPTFFPPYAPNPSVATPEDESMAPKPLESVVYQSN 60
1 MKIVLAIASLALSAVAVARPSSTPTFFPPYAPNPSVATPEDESMAPKPLESVVYQSN 60
61 GGAINHLSLSLEPPHFMGSAFAFEHLTPTFELMAFTNACSTUNAPAEIDLPMPYTV 120
61 GGAINHLSLSLEPPHFMGSAFAFEHLTPTFELMAFTNACSTUNAPAEIDLPMPYTV 120
121 TPIRMGGGSGSWAFSGVAATESAYLAVENGLMLAFORLWICASLSSPACTIPREIEY 180
121 TPIRMGGGSGSWAFSGVAATESAYLAVENGLMLAFORLWICASLSSPACTIPREIEY 180
181 IOHNVGSGSYYPVAFSGPPPPNAPQFQISNYCQIYPPNPNKIDELACTHSAIAVII 240
181 IOHNVGSGSYYPVAFSGPPPPNAPQFQISNYCQIYPPNPNKIDELACTHSAIAVII 240
241 GIKELDAFRHIGSTIIQPENGYFENHANNIVSTNSMAQSGVWIVRNSWETWJGNG 300
241 GIKELDAFRHIGSTIIQPENGYFENHANNIVSTNSMAQSGVWIVRNSWETWJGNG 300
301 YFAANIDUMMIEEYPYVIL 320
301 YFAANIDUMMIEEYPYVIL 315

RESULT 8

AA0498330

10 AA0498330 standard; Protein, 302 AA.

AA0498330;

21-AUG-2001 (first entry)

D. pteronyssinus Der p 1 protein fDer p1-302.

Mite group 1 protein, methylophilic yeast, Escherichia coli, allergy;
recombinant mite group 1 protein, allergic response, anti-allergic;
infectious disease, allergic disease.

Dermatophagoides pteronyssinus.

W020012708 A2.

26 APR 2001.

12 OCT 1999; 1999B-0118-04.

GenCore version 5.2.4 [5-1579
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ON PROTEIN PROPERTIES

Run on: May 11, 2003, 11:22:46, Sun Oct 19 07:44:55 Sun-03
(without alignments)
207.34 M1100.0 bit address 00

Title: US-09-877 1692

perfect score: 1689

Scoring table: 5000Mps
Gap: 10.0, Gap: 0.5

Searched: 188354 Sept. 1 1945

Total number of birds in population: 12,394

Minimum DB 500 10-12-14. 5

[illegible][illegible]

Year	Month	Day	Time	Location	Remarks
1900	March	10	10:30	St. Paul	Arrived at St. Paul
1900	March	11	11:00	St. Paul	Left St. Paul
1900	March	12	12:00	St. Paul	Arrived at St. Paul
1900	March	13	13:00	St. Paul	Left St. Paul
1900	March	14	14:00	St. Paul	Arrived at St. Paul
1900	March	15	15:00	St. Paul	Left St. Paul
1900	March	16	16:00	St. Paul	Arrived at St. Paul
1900	March	17	17:00	St. Paul	Left St. Paul
1900	March	18	18:00	St. Paul	Arrived at St. Paul
1900	March	19	19:00	St. Paul	Left St. Paul
1900	March	20	20:00	St. Paul	Arrived at St. Paul
1900	March	21	21:00	St. Paul	Left St. Paul
1900	March	22	22:00	St. Paul	Arrived at St. Paul
1900	March	23	23:00	St. Paul	Left St. Paul
1900	March	24	24:00	St. Paul	Arrived at St. Paul
1900	March	25	25:00	St. Paul	Left St. Paul
1900	March	26	26:00	St. Paul	Arrived at St. Paul
1900	March	27	27:00	St. Paul	Left St. Paul
1900	March	28	28:00	St. Paul	Arrived at St. Paul
1900	March	29	29:00	St. Paul	Left St. Paul
1900	March	30	30:00	St. Paul	Arrived at St. Paul

LASTING first 45 summaries

Database : Published Applications AA:*

- ```

1: /gnu-2/pdata/2/pdppaa/US00A NEW PUR REP:
2: /gnu-2/pdata/2/pdppaa/US00A NEW PUR REP:
3: /gnu-2/pdata/2/pdppaa/US00G NEW PUR REP:
4: /gnu-2/pdata/2/pdppaa/US00A PURCOMB REP:
5: /gnu-2/pdata/2/pdppaa/US00G NEW PUR REP:
6: /gnu-2/pdata/2/pdppaa/US00G PURCOMB REP:
7: /gnu-2/pdata/2/pdppaa/US00G PURCOMB REP:
8: /gnu-2/pdata/2/pdppaa/US00A PURCOMB REP:
9: /gnu-2/pdata/2/pdppaa/US00G NEW PUR REP:
10: /gnu-2/pdata/2/pdppaa/US00A PURCOMB REP:
11: /gnu-2/pdata/2/pdppaa/US00G NEW PUR REP:
12: /gnu-2/pdata/2/pdppaa/US00G PURCOMB REP:
13: /gnu-2/pdata/2/pdppaa/US00A NEW PUR REP:
14: /gnu-2/pdata/2/pdppaa/US00A PURCOMB REP:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID                 | Description        |
|------------|-------|-------------|--------|----|--------------------|--------------------|
| 1          | 1689  | 100.0       | 320    | 9  | US-09-993-160-2    | Sequence 2, Appl   |
| 2          | 36    | 2.4         | 324    | 10 | US-09-993-160-1    | Sequence 2, Appl   |
| 3          | 362   | 21.4        | 320    | 12 | US-10-114-454-2    | Sequence 2, Appl   |
| 4          | 362   | 22.4        | 322    | 12 | US-09-993-993-1633 | Sequence 833, Appl |
| 5          | 353   | 20.9        | 329    | 10 | US-09-993-993-7    | Sequence 7, Appl   |
| 6          | 355   | 20.5        | 329    | 12 | US-10-114-454-7    | Sequence 7, Appl   |
| 7          | 349   | 20.7        | 331    | 9  | US-09-993-044-3    | Sequence 2, Appl   |
| 8          | 349.5 | 20.5        | 328    | 10 | US-09-993-993-47M  | Sequence 47, Appl  |
| 9          | 333.5 | 19.7        | 335    | 10 | US-09-993-956-10   | Sequence 10, Appl  |
| 10         | 333.5 | 19.7        | 335    | 12 | US-10-114-454-7    | Sequence 1, Appl   |
| 11         | 325.5 | 19.3        | 331    | 10 | US-09-993-993-8    | Sequence 8, Appl   |
| 12         | 322.5 | 19.3        | 331    | 12 | US-10-114-454-8    | Sequence 4, Appl   |
| 13         | 318.5 | 18.9        | 331    | 9  | US-10-099-275-2    | Sequence 2, Appl   |
| 14         | 307.5 | 18.4        | 334    | 9  | US-10-143-511-1    | Sequence 1, Appl   |
| 15         | 305.5 | 18.2        | 334    | 9  | US-10-926-926-12   | Sequence 12, Appl  |
| 16         | 305.5 | 18.1        | 334    | 9  | US-10-123-123-12   | Sequence 12, Appl  |
| 17         | 305.5 | 18.1        | 334    | 9  | US-10-123-934-12   | Sequence 12, Appl  |
| 18         | 305.5 | 18.1        | 334    | 9  | US-10-143-474-12   | Sequence 12, Appl  |
| 19         | 305.5 | 18.1        | 334    | 9  | US-10-175-746-12   | Sequence 12, Appl  |

## ALIGNMENTS

```

RESULT 1
US 09 877-160-2
: Sequence 2, Application us/requsseq2
: Publication No. US000297319A1
: GENERAL INFORMATION:
:
: APPLICANT: Chiro Hwang, Han
: APPLICANT: Chiro Hwang, Han
: TITLE OF INVENTION: ALLERGEN CONTAINING W/IF FOR ALLERGY
: TITLE OF INVENTION: TREATMENT
: FILE REFERENCE: 127-4 6,2,11
: CURRENT APPLICATION NUMBER: us/0002973190
: CURRENT FILING DATE: 2001-06-08
: NUMBER OF SEQ ID NOS: 10
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 2
: LENGTH: 320
: TYPE: PRT
: ORGANISM: Dermatophagoides pteronyssinus
US-09-877-160-2

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Query Match 100.00; Score 1640; NP 9; Length 320;
Pos. Level: Similarity 100.00; P-Pos 7 to 160;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|    |   |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |     |          |
|----|---|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|
| 27 | 1 | WETULAKA | 124 | WETULAKA | 125 | WETULAKA | 126 | WETULAKA | 127 | WETULAKA | 128 | WETULAKA | 129 | WETULAKA | 130 | WETULAKA | 131 | WETULAKA | 132 | WETULAKA | 133 | WETULAKA | 134 | WETULAKA | 135 | WETULAKA | 136 | WETULAKA | 137 | WETULAKA | 138 | WETULAKA | 139 | WETULAKA | 140 | WETULAKA | 141 | WETULAKA | 142 | WETULAKA | 143 | WETULAKA | 144 | WETULAKA | 145 | WETULAKA | 146 | WETULAKA | 147 | WETULAKA | 148 | WETULAKA | 149 | WETULAKA | 150 | WETULAKA | 151 | WETULAKA | 152 | WETULAKA | 153 | WETULAKA | 154 | WETULAKA | 155 | WETULAKA | 156 | WETULAKA | 157 | WETULAKA | 158 | WETULAKA | 159 | WETULAKA | 160 | WETULAKA | 161 | WETULAKA | 162 | WETULAKA | 163 | WETULAKA | 164 | WETULAKA | 165 | WETULAKA | 166 | WETULAKA | 167 | WETULAKA | 168 | WETULAKA | 169 | WETULAKA | 170 | WETULAKA | 171 | WETULAKA | 172 | WETULAKA | 173 | WETULAKA | 174 | WETULAKA | 175 | WETULAKA | 176 | WETULAKA | 177 | WETULAKA | 178 | WETULAKA | 179 | WETULAKA | 180 | WETULAKA | 181 | WETULAKA | 182 | WETULAKA | 183 | WETULAKA | 184 | WETULAKA | 185 | WETULAKA | 186 | WETULAKA | 187 | WETULAKA | 188 | WETULAKA | 189 | WETULAKA | 190 | WETULAKA | 191 | WETULAKA | 192 | WETULAKA | 193 | WETULAKA | 194 | WETULAKA | 195 | WETULAKA | 196 | WETULAKA | 197 | WETULAKA | 198 | WETULAKA | 199 | WETULAKA | 200 | WETULAKA | 201 | WETULAKA | 202 | WETULAKA | 203 | WETULAKA | 204 | WETULAKA | 205 | WETULAKA | 206 | WETULAKA | 207 | WETULAKA | 208 | WETULAKA | 209 | WETULAKA | 210 | WETULAKA | 211 | WETULAKA | 212 | WETULAKA | 213 | WETULAKA | 214 | WETULAKA | 215 | WETULAKA | 216 | WETULAKA | 217 | WETULAKA | 218 | WETULAKA | 219 | WETULAKA | 220 | WETULAKA | 221 | WETULAKA | 222 | WETULAKA | 223 | WETULAKA | 224 | WETULAKA | 225 | WETULAKA | 226 | WETULAKA | 227 | WETULAKA | 228 | WETULAKA | 229 | WETULAKA | 230 | WETULAKA | 231 | WETULAKA | 232 | WETULAKA | 233 | WETULAKA | 234 | WETULAKA | 235 | WETULAKA | 236 | WETULAKA | 237 | WETULAKA | 238 | WETULAKA | 239 | WETULAKA | 240 | WETULAKA | 241 | WETULAKA | 242 | WETULAKA | 243 | WETULAKA | 244 | WETULAKA | 245 | WETULAKA | 246 | WETULAKA | 247 | WETULAKA | 248 | WETULAKA | 249 | WETULAKA | 250 | WETULAKA | 251 | WETULAKA | 252 | WETULAKA | 253 | WETULAKA | 254 | WETULAKA | 255 | WETULAKA | 256 | WETULAKA | 257 | WETULAKA | 258 | WETULAKA | 259 | WETULAKA | 260 | WETULAKA | 261 | WETULAKA | 262 | WETULAKA | 263 | WETULAKA | 264 | WETULAKA | 265 | WETULAKA | 266 | WETULAKA | 267 | WETULAKA | 268 | WETULAKA | 269 | WETULAKA | 270 | WETULAKA | 271 | WETULAKA | 272 | WETULAKA | 273 | WETULAKA | 274 | WETULAKA | 275 | WETULAKA | 276 | WETULAKA | 277 | WETULAKA | 278 | WETULAKA | 279 | WETULAKA | 280 | WETULAKA | 281 | WETULAKA | 282 | WETULAKA | 283 | WETULAKA | 284 | WETULAKA | 285 | WETULAKA | 286 | WETULAKA | 287 | WETULAKA | 288 | WETULAKA | 289 | WETULAKA | 290 | WETULAKA | 291 | WETULAKA | 292 | WETULAKA | 293 | WETULAKA | 294 | WETULAKA | 295 | WETULAKA | 296 | WETULAKA | 297 | WETULAKA | 298 | WETULAKA | 299 | WETULAKA | 300 | WETULAKA | 301 | WETULAKA | 302 | WETULAKA | 303 | WETULAKA | 304 | WETULAKA | 305 | WETULAKA | 306 | WETULAKA | 307 | WETULAKA | 308 | WETULAKA | 309 | WETULAKA | 310 | WETULAKA | 311 | WETULAKA | 312 | WETULAKA | 313 | WETULAKA | 314 | WETULAKA | 315 | WETULAKA | 316 | WETULAKA | 317 | WETULAKA | 318 | WETULAKA | 319 | WETULAKA | 320 | WETULAKA | 321 | WETULAKA | 322 | WETULAKA | 323 | WETULAKA | 324 | WETULAKA | 325 | WETULAKA | 326 | WETULAKA |
|----|---|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|-----|----------|



















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RESULT 2
QBOWKS
ID CQCKFS PRELIMINARY EST 109 AA.
AC Q8WOKS
DI 01-MAR-2001 (REMBRel_19, Created)
DT 01-MAR-2002 (IREMBRel_20, Last sequence update)
DE 01-JUN-2002 (IEMBLrel_21, Last annotation update)
MAJor Der f 2 isoform (Fragment).
OS Dermatophagoides farinae (House dust mite)
OC Eukaryota, Metazoa, Arthropoda; Chelicerata; Arachnida; Acari;
OC Acariformes; Sarcoptiformes; Astigmata; Amblyosoma, Pyroglyphidae,
OC Dermatophagoides.
OC NCPI_TaxID=6954;
RN [1]
RP SEQUENCE FROM N.A.
RA Jin H.S., Oh S.H., Hong G.S.:
RA "cDNA sequence encoding major Der f 2 isoform in Korea."
RA Submitted (DEC-2001), to the EMBL/GenBank/CCDB databases
PP EMBL: AY066009; AAL47677.1; -
DP InterPro: IPR003172, El_Derf2_DerF2.
DR Pfam: PF02221, El_Derf2_DerF2; 1.
FT NON TER 1
SQ SEQUENCE 109 AA, 14336 MW, 822FCEDCEIEHIF CRG64,
Query Match 80.9%, Score 625, DB 5, Length 109,
Best Local Similarity 97.6%; Prod.NC.1.2e-19;
Matches 112, Conservative 12, Mismatches 4, Indels 0; Gaps 0;
CQ 1A TCGTCCTATHEITPVVVFCSHSSETHHPDFFQLFAVFEAAAGTPTAFETIASIS 77
LP 1 GVGVNVTATHEIPAVMVEYVSTGGP-IHP-DHTLEALFDANLTPTAFETIASIS 69
CY 1A LFGNTQTGNATHMPTRGFSDCTPHFTTWVPYTIAPSENVVTVVTFIVLAIA 137
DB 61 LDPAEADNTAHFMPEWPFEGGTAFITWTMTPTAPSCNVTVTVDSPVLACA 100
OZ 109 LATHAFIED 146
DB 121 LATHAKID 129
RESULT 3
Q965E2
ID CQKSED PRELIMINARY, EST, 143 AA.
AC CQKDED
DI 01-DEC-2001 (REMBRel_19, created)
DT 01-SEP-2001 (IREMBRel_19, Last sequence update)
DE 01-MAR-2002 (IREMBRel_20, Last annotation update);
OS Psocoptes.
DE Allergen A precursor.
AC ALGA.
OS Psocoptes ovis (sheep scab mite).
OC Eukaryota, Metazoa, Arthropoda, Chelicerata, Arachnida, Acari.
OC Acarifurcata; Sarcoptiformes; Astigmata, Sarcoptidae, Psocoptidae.
OC Psocoptes.
OX NCPI_TaxID=81012;
RN [1]
RP SEQUENCE FROM N.A.
RA Temeyer K.B., Soileau L.C.:
RA "Sequence of a cDNA encoding a precursor of a major allergen of
RA Psocoptes ovis."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EVR6, AR1809, AAA18234.1.
DR InterPro: IPP004172, El_DerF2_DerF2.
DR Pfam: PF02221, El_DerF2_DerF2; 1.
Signal.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 16 143 ALLERGEN A.
SQ SEQUENCE 143 AA, 15312 MW, AFRTAASGSGPAAAAD CPK64;
Query Match 39.7%; Score 306.5; DB 5; Length 143;
Best Local Similarity 77.0%; Prod.NC.1.9e-05;

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RX MEDLINE=2113526; PubMed=11240953;  
 RA Gaivelin G., Johansson E., Lundin A., Smith A.M., Chapman M.D.,  
 RA Reinhold D., Cretzschmar H., van Hage-Hamgren M.,  
 RT "Cross reactivity studies of a new group 2 allergen from the dust mite  
 RT Glycyphagus domesticus, Gly d 2, and group 2 allergens from  
 RT Dermatophagoides pteronyssinus, Lepidoglyphus destructor, and  
 RT Tyroglyphus putrescentiae with recombinant allergens",  
 RJ J. Allergy Clin. Immunol. 107:511-518(2001).  
 DR PMID: 1124424; AAF54472.1;  
 DR HSP; Q00855; IAHK.  
 DR InterPro: IPR001172; E1\_DerP2\_DerP2  
 DR Pfam: PF02221; E1\_DerP2\_DerP2.1.  
 FT NON\_TER 1  
 SQ SEQUENCE 128 AA; 13790 MW; 431A027F589A7E03 CRC64;  
 Query Match 32.2%; Score 249; DB 5; Length 128;  
 Best Local Similarity 40.5%; Pred. No. 1e-18;  
 Matches 49; Conservative 11; Mismatches 35; Indels 6; Gaps 4;  
 QY 10 CVTVFZANHEIFVYVTSCHDEFFTHIEFFLEAVFAVQVDTTAFIEFAS103 11  
 DB 2 KMSFTSCHEHPELSEVETGNYGVHESFILLFAFPAH134VNVNHAH115 12  
 QY 78 LEVDVGVGIGENACHVWQELVWQVQVYKVTWVVKIAPKSENVVTVK--VMGDSGVLA 135  
 DB 61 IADIDFENLACNACVNFCTIFGEGCELYI KGEIFGATPEIFAPVFA135EHSVLA 139  
 QY 136 C 136  
 DB 119 C 119  
 RESULT 5  
 Q17271 PRELIMINARY; PRT: 186 AA.  
 AC Q17271;  
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 14, Last annotation update)  
 DE Hypothetical 20.3 kDa protein.  
 GN R148.6.  
 OS Caenorhabditis elegans  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Phabditida; Phabditidae;  
 OC Rhabditidae; Rhabditinae; Caenorhabditis.  
 QY 119 TIVN-6299;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRISTOL N2;  
 RX MEDLINE=99565613; PubMed=9651915;  
 RA None;  
 RT "Genome sequence of the nematode C. elegans: a platform for  
 RT investigating biology. The C. elegans Sequencing Consortium";  
 RL Science 282:2155-2159(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRISTOL N2;  
 RA Le Tiff., Fari F., Schatz P.,  
 RT "The sequence of C. elegans cosmid R148.",  
 RL Submitted (1997) to the EMBL/GenBank/DBJ databases  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRISTOL N2;  
 RA Waterston R.,  
 RT "Direct Submission";  
 RL Submitted (2001) to the EMBL/GenBank/DBJ databases  
 DR PMID: 1124424; AAF54472.1;  
 DR InterPro: IPR001172; E1\_DerP2\_DerP2  
 DR Pfam: PF02221; E1\_DerP2\_DerP2.1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 186 AA; 20640 MW; 7AF6927CAF58FAC3 CRC64;  
 Query Match 14.9%; Score 115.5; DB 5; Length 186;  
 Best Local Similarity 21.4%; Pred. No. 6.6e-64.

Matches 36; Conservative 38; Mismatches 71; Indels 9; Gaps 5;  
 QY 4 MYKLLLSLL VAAVAP-ATVKEP-ANHEKRVLP-CH-----GSEGLIHAGKATQL 54  
 DB 11 MTVFIFALL-IAAAEFIEI-YFV FVSTV-IVAGT-ETVFGAPV-IVAGAPFI 92  
 QY 55 EAVFATGTTTATFIEFASIS LEVVFQIEFNACHY MEETLVNDEQVQVITNNVP 112  
 DB 53 GAFFESKTELEFTS-VPAFV-NAAMVFF-JN-FA-TW-VFV-IVAGT-ETVFGAPFI 154  
 QY 113 KAPKSENVVTVVWVGQGVGLACALAHAKIRD 146  
 DB 153 ENHPAGEVIQNNQUTRDSDKEVCIIFLAEIKE 186  
 RESULT 7  
 Q9VH31 PRELIMINARY; PRT: 155 AA.  
 ID Q9VH31;  
 AC Q9VH31;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 14, Last annotation update)  
 DE CG3934 protein.  
 DB CG3934.  
 GN Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY;  
 RX MEDLINE=20196006; PubMed=10721132;  
 RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.P., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 RA Wan H., Doyle S., Baxter E., Heit R., Nelson J.F., Mitkus G.L.G.,  
 RA Abell J.F., Agtayan A., An H.J., Andrews-Ffankoch C., Baldwin D.,  
 RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berns P.P., Bhandari D., Bolshakov S.,  
 RA Borstova D., Borchan M.P., Brown J., Bruckner P., Brucher P.,  
 RA Burlis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cwikley S., Dahlke C., Davernport L.B., Davies P.,  
 RA de Paabes B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Eup L.E., Fowler M., Dugan Pocha S., Dunkey B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Fettieta S., Fleischman W.,  
 RA Foster C., Gabrielson A.E., Garg N.S., Gehart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.P., Houck J.,  
 RA Heston D., Houston V.A., Howland T.J., Wei M.H., Ibegwan C.,  
 RA Jialili M., Kalish J., Kainer G.H., Ke S., Kennedy J.A., Ketchum T.A.,  
 RA Kimmel P.P., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Morfoll G., Mulkaira V., Murphy A., Norris J., Koshire A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.P., Nelson F.A., Niz J.P., Nuskett C.F., Paclet J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Peibert K., Penington K., Saunders P.C., Scheeler P., Shen H.,  
 RA Shie B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.Y., Wasserman D.A., Weinschenk G.M., Weissbach J.,  
 RA Williams S.M., Woodage J., Worley K., Wu E., Yang S., Yao Q.A.,  
 RA Ye J., Yeh P.F., Zaveri J.C., Zhan M., Zhao C., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 FT "The genome sequence of Drosophila melanogaster";  
 RL Science 287:2185-2195(2000).  
 DR EMBL: AB003685; AAF54469.1;  
 DE FlyBase: FBgn037783; CG3934.

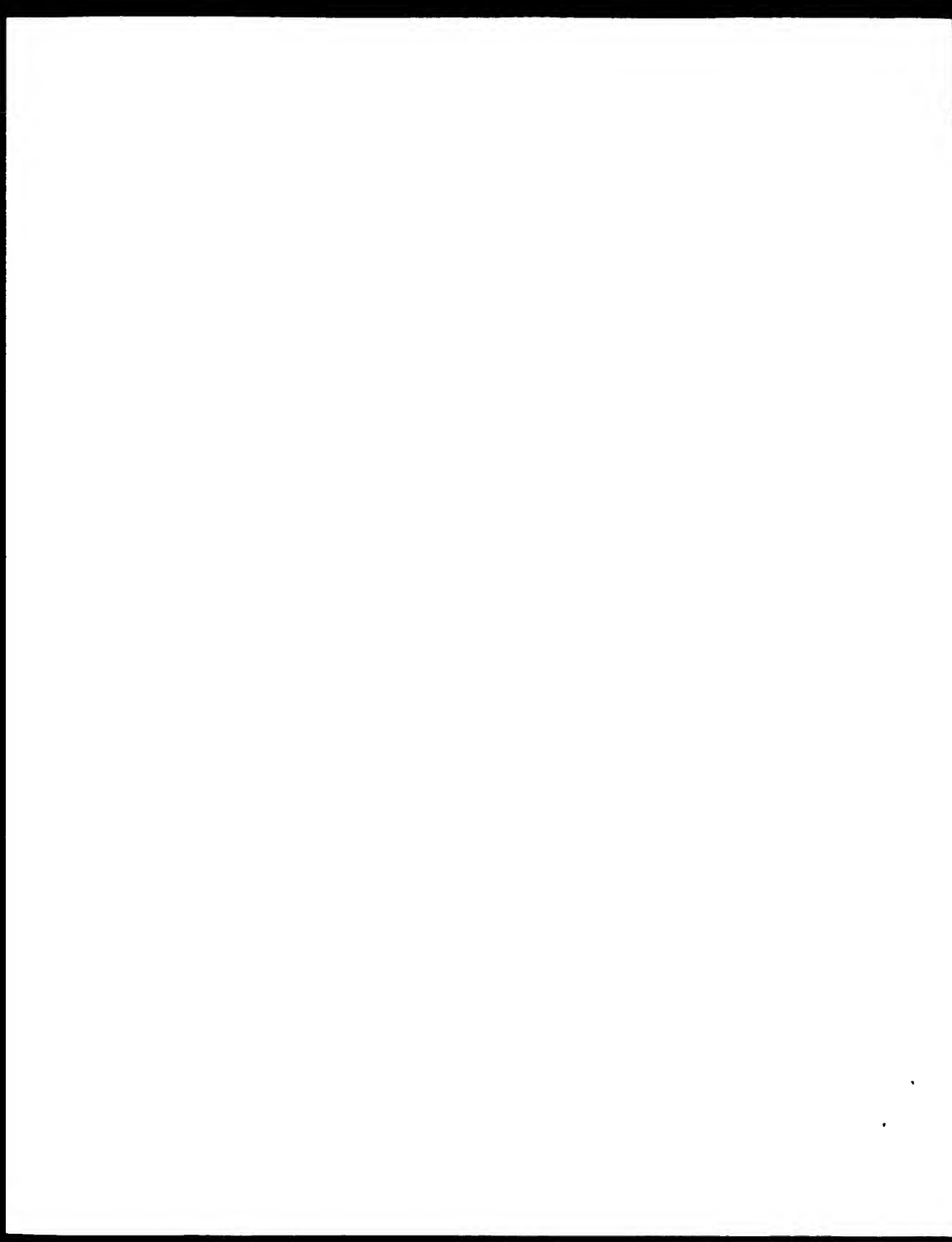
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OM protein Protein search, using sw model

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(without alignments)  
527,709 Million cell updates/sec

Title: US-09-877-160-3

Perfect score: 773

Sequence: 1 MWYFICLSLAIAVARETV.....VMSGVGLACIAIAHAFVIE 146

Scoring tables: BLASTW2

Gapop 10.0, Gapext 0.5

Searched: 208470 seqs, 13320220 residues 98470

Total number of hits satisfying chosen parameters

Minimum DB seq length: 0

Maximum DB seq length: 1000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: 1 A\_Geneseq\_101002 \*

|     |                                                  |
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| 1:  | /SID22/gcgdata/geneseq/geneseq_emb1/AA1981.DAT * |
| 2:  | /SID22/gcgdata/geneseq/geneseq_emb1/AA1981.DAT * |
| 3:  | /SID22/gcgdata/geneseq/geneseq_emb1/AA1982.DAT * |
| 4:  | /SID22/gcgdata/geneseq/geneseq_emb1/AA1983.DAT * |
| 5:  | /SID22/gcgdata/geneseq/geneseq_emb1/AA1984.DAT * |
| 6:  | /SID22/gcgdata/geneseq/geneseq_emb1/AA1985.DAT * |
| 7:  | /SID22/gcgdata/geneseq/geneseq_emb1/AA1986.DAT * |
| 8:  | /SID22/gcgdata/geneseq/geneseq_emb1/AA1987.DAT * |
| 9:  | /SID22/gcgdata/geneseq/geneseq_emb1/AA1988.DAT * |
| 10: | /SID22/gcgdata/geneseq/geneseq_emb1/AA1989.DAT * |
| 11: | /SID22/gcgdata/geneseq/geneseq_emb1/AA1990.DAT * |
| 12: | /SID22/gcgdata/geneseq/geneseq_emb1/AA1991.DAT * |
| 13: | /SID22/gcgdata/geneseq/geneseq_emb1/AA1992.DAT * |
| 14: | /SID22/gcgdata/geneseq/geneseq_emb1/AA1993.DAT * |
| 15: | /SID22/gcgdata/geneseq/geneseq_emb1/AA1994.DAT * |
| 16: | /SID22/gcgdata/geneseq/geneseq_emb1/AA1995.DAT * |
| 17: | /SID22/gcgdata/geneseq/geneseq_emb1/AA1996.DAT * |
| 18: | /SID22/gcgdata/geneseq/geneseq_emb1/AA1997.DAT * |
| 19: | /SID22/gcgdata/geneseq/geneseq_emb1/AA1998.DAT * |
| 20: | /SID22/gcgdata/geneseq/geneseq_emb1/AA1999.DAT * |
| 21: | /SID22/gcgdata/geneseq/geneseq_emb1/AA2000.DAT * |
| 22: | /SID22/gcgdata/geneseq/geneseq_emb1/AA2001.DAT * |
| 23: | /SID22/gcgdata/geneseq/geneseq_emb1/AA2002.DAT * |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length DB | ID       | Description        |
|------------|-------|-------------|-----------|----------|--------------------|
| 1          | 773   | 100.0       | 146       | AA191060 | Dermatophagoides p |
| 2          | 773   | 100.0       | 146       | AA191728 | Der p II, Dermato  |
| 3          | 773   | 100.0       | 146       | AA191909 | Dermatophagoides f |
| 4          | 773   | 100.0       | 146       | AA191957 | Dermatophagoides s |
| 5          | 773   | 100.0       | 146       | AA192581 | D. pteronyssinus a |
| 6          | 773   | 100.0       | 146       | AA191860 | House dust mite al |
| 7          | 773   | 100.0       | 146       | AA191860 | House dust mite al |
| 8          | 773   | 100.0       | 146       | AA191860 | House dust mite al |
| 9          | 758   | 98.1        | 145       | AA191860 | Protein allergen o |
| 10         | 755   | 97.7        | 145       | AA191860 | Der p II antigen f |

|    |     |      |     |    |          |                     |
|----|-----|------|-----|----|----------|---------------------|
| 11 | 693 | 99.7 | 129 | 23 | ABG66997 | House dust mite al  |
| 12 | 690 | 99.3 | 129 | 23 | ABG67001 | House dust mite al  |
| 13 | 689 | 99.1 | 129 | 23 | AA191860 | House dust mite al  |
| 14 | 689 | 99.1 | 129 | 23 | ABG78996 | House dust mite al  |
| 15 | 689 | 99.1 | 129 | 23 | ABG66972 | House dust mite al  |
| 16 | 689 | 99.1 | 129 | 23 | ABG66991 | House dust mite al  |
| 17 | 689 | 99.1 | 129 | 23 | ABG66995 | House dust mite al  |
| 18 | 689 | 99.1 | 129 | 23 | ABG67000 | House dust mite al  |
| 19 | 689 | 99.1 | 129 | 23 | ABG67009 | House dust mite al  |
| 20 | 689 | 99.0 | 129 | 23 | ABG66971 | House dust mite al  |
| 21 | 688 | 99.0 | 129 | 23 | ABG66976 | House dust mite al  |
| 22 | 688 | 99.0 | 129 | 23 | ABG66999 | House dust mite al  |
| 23 | 688 | 99.0 | 129 | 23 | ABG67004 | House dust mite al  |
| 24 | 688 | 99.0 | 129 | 23 | ABG67006 | House dust mite al  |
| 25 | 688 | 99.0 | 129 | 23 | ABG67007 | House dust mite al  |
| 26 | 688 | 99.0 | 129 | 23 | ABG67009 | House dust mite al  |
| 27 | 687 | 98.9 | 129 | 23 | ABG66971 | House dust mite al  |
| 28 | 687 | 98.9 | 129 | 23 | ABG66998 | House dust mite al  |
| 29 | 687 | 98.9 | 129 | 23 | ABG67002 | House dust mite al  |
| 30 | 687 | 98.9 | 146 | 20 | AA192589 | D. farinae allergen |
| 31 | 686 | 98.7 | 129 | 23 | ABG66973 | House dust mite al  |
| 32 | 686 | 98.7 | 129 | 23 | ABG66975 | House dust mite al  |
| 33 | 686 | 98.7 | 129 | 23 | ABG66992 | House dust mite al  |
| 34 | 686 | 98.7 | 129 | 23 | ABG66994 | House dust mite al  |
| 35 | 686 | 98.7 | 129 | 23 | ABG67005 | House dust mite al  |
| 36 | 686 | 98.6 | 129 | 23 | ABG66992 | House dust mite al  |
| 37 | 684 | 98.5 | 129 | 23 | ABG66994 | House dust mite al  |
| 38 | 681 | 98.1 | 129 | 23 | ABG66996 | House dust mite al  |
| 39 | 680 | 98.0 | 129 | 23 | ABG66994 | House dust mite al  |
| 40 | 678 | 87.7 | 129 | 15 | AA191921 | Protein allergen o  |
| 41 | 674 | 87.7 | 129 | 15 | AA191922 | Protein allergen o  |
| 42 | 674 | 87.7 | 129 | 15 | AA191923 | Protein allergen o  |
| 43 | 673 | 87.0 | 142 | 12 | AA191984 | House dust mite al  |
| 44 | 654 | 84.6 | 142 | 12 | AA191984 | Der p II allergen e |
| 45 | 653 | 84.5 | 142 | 12 | AA191984 | Der p II allergen e |

#### ALIGNMENTS

RESULT 1  
AAR39360  
ID AAR39360 standard, Protein, 146 AA.  
XX  
XX AAR39360  
XX  
XX 12 AUG 1993 (first entry)  
XX  
XX Dermatophagoides pteronyssinus Dep pII.  
XX  
XX T cell epitope, house dust mite, allergen, soluble; allergen.  
XX  
XX Dermatophagoides pteronyssinus.  
XX  
XX WO9108279-A.  
XX  
XX 29-APR-1993.  
XX  
XX 15-OCT-1992; 92WO-US08637.  
XX  
XX 16-OCT-1991; 91US-0717459.  
XX  
XX 08-MAY-1992; 92US-0841596.  
XX  
XX (IMMU-) IMMLOGIC PHARM CORP.  
XX  
XX Garman PD, Greenstein JL, Kuc MC, Rogers BL;  
XX  
XX WPI: 1993-152472/18.  
XX  
XX H FSEB, C41113.  
XX  
XX Isolated peptide(s) of Dermatophagoides protein allergens for  
XX  
XX diagnosis and treatment of sensitivity to house dust mite

PS Disclosure, Page 42, 170pp, English.

XX The cDNA encoding Dermatophagoides pteronyssinus group II allergen  
CC Dep pII was obtained in plasmid form as subclone from lambda gt11 (Chua  
CC et al., Int Arch Allergy Immun 110:123 (1994)). The cDNA was used to  
CC express a Dep pII allergen capable of raising an immune response when  
CC contacted with anti Dep pII antibodies. The protein was used to design  
CC a series of overlapping peptides synthesized by standard techniques to  
CC cover the whole Dermatophagoides pteronyssinus Dep pII sequence. The  
CC cell epitopes of the protein were mapped by detection of the peptides  
CC ability to stimulate T cell activity. The peptides may be used for  
CC diagnosis and treatment of sensitivity to house dust mite allergens  
CC When administered to house dust mite sensitive individuals, the  
CC peptides are capable of modifying the allergic response to the  
CC allergens. The peptides may be modified for e.g. increasing solubility,  
CC enhancing therapeutic or preventive efficacy or stability.  
XX See also NAPSDB: 435, AAR51728 435 and AAR51729 435

XX Sequence 146 AA.

Query Match 100.0%; Score 773; DP 14; Length 146;

Best Local Similarity 100.0%; Pred. No. 1.5e-85;

Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1 MWYVLLLSLLVAARQGVVLELVAARHEIPKVLVLEHSENCITHEPPTPEAVPEA 60

DB 1 MWYVLLLSLLVAARQGVVLELVAARHEIPKVLVLEHSENCITHEPPTPEAVPEA 60

QY 61 NQNTYAKHEIFASIPSEFVTVVPTGPDNAQHWGTPLVK 50

DB 61 NQNTYAKHEIFASIPSEFVTVVPTGPDNAQHWGTPLVK 50

QY 121 VVTVVVMGSDGVLACAIATHAKIPD 146

DB 121 VVTVVVMGSDGVLACAIATHAKIPD 146

QY 121 VVTVVVMGSDGVLACAIATHAKIPD 146

DB 121 VVTVVVMGSDGVLACAIATHAKIPD 146

QY 121 VVTVVVMGSDGVLACAIATHAKIPD 146

DB 121 VVTVVVMGSDGVLACAIATHAKIPD 146

QY 121 VVTVVVMGSDGVLACAIATHAKIPD 146

DB 121 VVTVVVMGSDGVLACAIATHAKIPD 146

QY 121 VVTVVVMGSDGVLACAIATHAKIPD 146

DB 121 VVTVVVMGSDGVLACAIATHAKIPD 146

QY 121 VVTVVVMGSDGVLACAIATHAKIPD 146

DB 121 VVTVVVMGSDGVLACAIATHAKIPD 146

QY 121 VVTVVVMGSDGVLACAIATHAKIPD 146

DB 121 VVTVVVMGSDGVLACAIATHAKIPD 146

QY 121 VVTVVVMGSDGVLACAIATHAKIPD 146

DB 121 VVTVVVMGSDGVLACAIATHAKIPD 146

QY 121 VVTVVVMGSDGVLACAIATHAKIPD 146

DB 121 VVTVVVMGSDGVLACAIATHAKIPD 146

QY 121 VVTVVVMGSDGVLACAIATHAKIPD 146

DB 121 VVTVVVMGSDGVLACAIATHAKIPD 146

QY 121 VVTVVVMGSDGVLACAIATHAKIPD 146

DB 121 VVTVVVMGSDGVLACAIATHAKIPD 146

QY 121 VVTVVVMGSDGVLACAIATHAKIPD 146

DB 121 VVTVVVMGSDGVLACAIATHAKIPD 146

QY 121 VVTVVVMGSDGVLACAIATHAKIPD 146

DB 121 VVTVVVMGSDGVLACAIATHAKIPD 146

QY 121 VVTVVVMGSDGVLACAIATHAKIPD 146

DB 121 VVTVVVMGSDGVLACAIATHAKIPD 146

QY 121 VVTVVVMGSDGVLACAIATHAKIPD 146

DB 121 VVTVVVMGSDGVLACAIATHAKIPD 146

PT Isolated and/or modified peptides comprising T cell epitopes of  
PT major protein allergens of genus Dermatophagoides, used to treat  
XX or diagnose sensitivity to house dust mites  
XX Disclosure: Page 42, 170pp, English.

XX This sequence represents the group II protein allergen from the house  
XX dust mite D. pteronyssinus, Der p II. The Der p II protein shows high  
XX homology to the group II protein allergen derived from D. farinose, Der  
XX f II, having an identity of 84%. Fragments of these proteins, and the  
XX corresponding group I allergens, Der p I and Der f I, (see AAR5171-841)  
XX represent T-cell epitopes. Further epitopes may be produced which  
XX comprise at least two or three antigenic fragments. Each region of these  
XX peptides may be derived from the same, or different, amino acid  
XX antigenic fragments may be altered by substitution, deletion or addition  
XX to enhance their antigenicity. These peptides may be produced by  
XX chemical synthesis, chemical cleavage of the protein allergen or by  
XX recombinant techniques. These peptides, when administered to a house  
XX dust mite sensitive individual, are capable of modifying the allergic  
XX response of the individual to the allergen. These peptides do not bind  
XX to immunoglobulin E (IgE), or bind IgE to a lesser extent than the full  
XX length protein allergen. This reduces the major complications of  
XX standard immunotherapy, which are IgE-mediated responses such as  
XX anaphylaxis. Exposure of mite allergic patients to these peptides may  
XX relieve or ameliorate symptoms of mite sensitivity such that they  
XX become unresponsive to mite allergens and do not participate in mounting  
XX an immune response against mite allergens. Administration of the peptides may  
XX also modify the lymphokine secretion profile as compared with exposure  
XX to the naturally occurring mite protein allergen.

XX Sequence 146 AA.

Query Match 100.0%; Score 773; DP 14; Length 146;

Best Local Similarity 100.0%; Pred. No. 1.5e-85;

Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1 MWYVLLLSLLVAARQGVVLELVAARHEIPKVLVLEHSENCITHEPPTPEAVPEA 60

DB 1 MWYVLLLSLLVAARQGVVLELVAARHEIPKVLVLEHSENCITHEPPTPEAVPEA 60

QY 61 NQNTYAKHEIFASIPSEFVTVVPTGPDNAQHWGTPLVK 50

DB 61 NQNTYAKHEIFASIPSEFVTVVPTGPDNAQHWGTPLVK 50

QY 121 VVTVVVMGSDGVLACAIATHAKIPD 146

DB 121 VVTVVVMGSDGVLACAIATHAKIPD 146

RESULT 3

AAW71909

ID AAW71909 standard; Protein; 146 AA.

XX AAW71909;

AC AAW71909;

XX 16-DEC-1998 (first entry)

DT 16-DEC-1998 (first entry)

XX Dermatophagoides Der p II.

DE Dermatophagoides Der p II.

XX Genus Dermatophagoides; Major Protein Allergen; T cell epitopes;

FW Der p I, Der p II, Der f I, Der f II, Der f III, Der f IV, Der f V,

XX Dermatophagoides sp.

OS Dermatophagoides sp.

XX US9502862-A.

PN 13-OCT-1998.

XX 07-JUN-1998; GMS-042142.

PP 15-MAY-1995; 95US-0445307.

XX 14-APR-1994; 94US-0227772.

PR 07-JUN-1995; 95US-0492142.

XX Garman PD, Greenstein JL, Kuo M, Rogers RL;

XX WPI; 1994-128907/15.

DR N-PSDB; MAQ62109.

XX (IMMU-) IMMUNOLOGIC PHARM CORP.











## RESULT 11

ABG66997  
ID ABG66997 Standard; Protein: 129 AA.

XX AC ABG66997;

XX DT 24 SEP 2002 (first entry)

XX XX House dust mite allergen Der p 2 ALK-114

XX KW Immunoglobulin E, IgE, allergen, allergy, hay fever,  
XX KW rhinoconjunctivitis, rhinitis, asthma, systemic anaphylaxis;  
XX KW vaccine, antiallergic, B cell epitope

XX CC Dermatophagoides pteronyssinus.

XX PN WC200240676-A2.

XX PD 23 MAY 2002.

XX FF 16 NOV 2001; 2001WV-DK00764.

XX PP 16 NOV 2000; 2000UK-0001718

XX PR 16 NOV 2000; 2000US-244461P

XX PP 14 JUN 2001; 2001US-298170P.

XX PA (ALKA-) ALK-ABELLO AS.

XX PI Holm J, Ipsen H, Nedergaard Larsen J, Spangfort MD;

XX VY WPI; 2002-508328/54.

XX DR N-PSNR: AR65425

XX PT New recombinant mutant allergen, useful for preventing and/or treating

XX PT allergy, comprises multiple mutations and reduced immunoglobulin E

XX PT binding affinity

XX XX Example 5; Page 91; 210pp; English.

XX CC The invention relates to a recombinant allergen (I) which is a mutant of  
CC a naturally occurring allergen, where the mutant allergen has at least  
CC four primary mutations, which each reduce the specific immunoglobulin E  
CC (IgE) binding capability of the mutated allergen as compared to the IgE  
CC binding capability of the naturally occurring allergen, where each  
CC primary mutation is a substitution of one surface exposed amino acid  
CC residue with another residue, which does not occur in the same position  
CC in the amino acid sequence of any known homologous protein within the  
CC taxonomic species from which the naturally occurring allergen  
CC originates, and each primary mutation is spaced from each other primary  
CC mutation by at least 15 Angstrom, and the primary mutations are placed  
CC in such a manner that at least one circular surface region with a area  
CC of 800 Angstrom<sup>2</sup> comprises no mutation. Also included are a composition  
CC comprising two or more of the recombinant allergens, where the variant  
CC allergen is defined by having at least one primary mutation, which is  
CC absent in at least one of the other variants, and for each variant no  
CC secondary mutation is present within a radius of 15 Angstrom from each  
CC absent primary mutation; a DNA sequence encoding the recombinant allergen  
CC or its derivative, partial sequence or degenerated sequence, or a  
CC sequence which hybridises to it under stringent conditions, where the  
CC derivative, partial sequence, degenerated sequence or hybridising  
CC sequence encodes a peptide having at least one B cell epitope; an  
CC expression vector comprising the DNA and a host cell comprising the  
CC vector. The recombinant allergen is useful as a pharmaceutical, for  
CC preparing a pharmaceutical for preventing and/or treating allergy, or in  
CC a diagnostic assay for assessing relevance, safety or outcome of therapy  
CC of a subject, where an IgE containing sample of the subject is mixed  
CC with the recombinant allergen and assessed for the level of reactivity  
CC between the IgE in the sample and the recombinant allergen. The  
CC recombinant allergen or compositions are useful for generating an  
CC immune response in a subject, for vaccination or treatment of a subject  
CC or for the treatment, prevention or alleviation of allergic reactions  
CC in a subject e.g. hay fever, rhinoconjunctivitis, rhinitis, asthma or  
CC systemic anaphylaxis. The present application relates to a composition

CC allergen of the invention.

XX SQ Sequence 129 AA;

XX Query Match 99.71; Score 693; DB 23; Length 129;

XX Best Local Similarity 100.00; Pident. No. 6.6e-76;

XX Matches 129; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

XX QY 18 EQVLYVTACHIEFFVVLVSESESEIITTHKSPFQSLZAKPEACQKTKETAFIEKASLIG 77

XX DL 1 EQVDVVTACHIEFFVVLVSESESEIITTHKSPFQSLZAKPEACQKTKETAFIEKASLIG 60

XX QY 78 LEVTVFRTFENATHTMWPTEIYVQSLQSLITVYWRVQFIAPSENWVTVVWVWDEQVLACA 137

XX DL 6 LEVTVFRTFENATHTMWPTEIYVQSLQSLITVYWRVQFIAPSENWVTVVWVWDEQVLACA 120

XX QY 138 IATHAKIRD 146

XX DL 121 IATHAKIRD 129

## RESULT 12

ABG67001

XX ID ABG67001 Standard; Protein: 129 AA.

XX AC ABG67001;

XX XX 24 SEP 2002 (first entry)

XX DE House dust mite allergen Der p 2 ALK-114 mutant S24N

XX KW Immunoglobulin E, IgE, allergen, allergy, vaccine, hay fever;

XX KW rhinoconjunctivitis, rhinitis, asthma, systemic anaphylaxis; mutant;

XX KW vaccine, antiallergic, B cell epitope.

XX CC Dermatophagoides pteronyssinus.

XX CS Synthetic.

XX XX WC200240676-A2.

XX XX 23 MAY 2002.

XX FF 16 NOV 2001; 2001WE-DE03754.

XX XX 16 NOV 2000; 2000UK-0001719.

XX PP 16 NOV 2000; 2000US-244461P.

XX PP 14 JUN 2001; 2001US-298170P.

XX PA (ALKA-) ALK-ABELLO AS.

XX PI Holm J, Ipsen H, Nedergaard Larsen J, Spangfort MD;

XX VY WPI; 2002-508328/54.

XX DE New recombinant mutant allergen, useful for preventing and/or treating

XX DE allergy, comprises multiple mutations and reduced immunoglobulin E

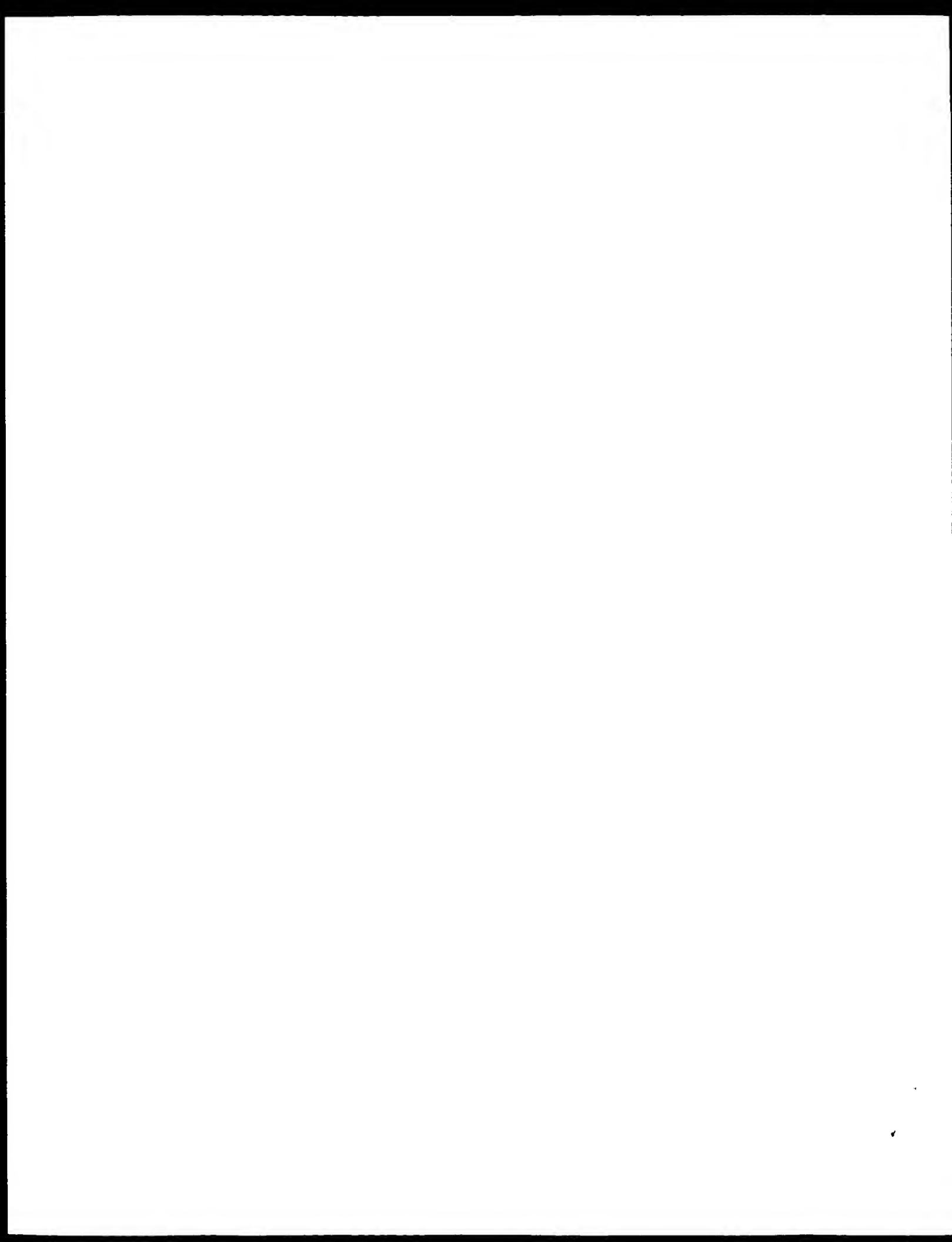
XX DE binding affinity

XX PS Example 6; Page 91; 210pp; English.

XX CC The invention relates to a recombinant allergen (I) which is a mutant of  
CC a naturally occurring allergen, where the mutant allergen has at least  
CC four primary mutations, which each reduce the specific immunoglobulin E  
CC (IgE) binding capability of the mutated allergen as compared to the IgE  
CC binding capability of the naturally occurring allergen, where each  
CC primary mutation is a substitution of one surface exposed amino acid  
CC residue with another residue, which does not occur in the same position  
CC in the amino acid sequence of any known homologous protein within the  
CC taxonomic species from which the naturally occurring allergen  
CC originates, and each primary mutation is spaced from each other primary  
CC mutation by at least 15 Angstrom, and the primary mutations are placed  
CC in such a manner that at least one circular surface region with a area  
CC of 800 Angstrom<sup>2</sup> comprises no mutation. Also included are a composition









; APPLICANT: CONSILIO NAZIONALE DELLE PIERCE  
 ; TITLE OF INVENTION: VARIANTS OF ALLERGENIC PROTEINS OF THE GROUP 2 OF  
 ; FILE REFERENCE: DERMATOPHAGOIDES  
 ; CURRENT FILING DATE: 2001/09/12  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: Patent In Ver. 2.1  
 ; SEQ ID NO 3  
 ; LENGTH: 145  
 ; TYPE: PRT  
 ; ORGANISM: Dermaphagoides pteromyssinus  
 US-09-949-889-3

Query Match 94.5%; Score 653; DB 10; Length 129;  
 Best Local Similarity 94.6%; Pred. No. 5,7e-67;  
 Matches 122; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

C1 MYKILICSLVAVARQVAVESCAHEIFVAVGCHCEPFIHFQKFFLEAVFAN 61  
 DB 1 MYKILICSLVAVARQVAVESCAHEIFVAVGCHCEPFIHFQKFFLEAVFAN 61  
 C2 MYKILICSLVAVARQVAVESCAHEIFVAVGCHCEPFIHFQKFFLEAVFAN 121  
 DB 1 MYKILICSLVAVARQVAVESCAHEIFVAVGCHCEPFIHFQKFFLEAVFAN 121  
 C3 MYKILICSLVAVARQVAVESCAHEIFVAVGCHCEPFIHFQKFFLEAVFAN 145  
 DB 1 MYKILICSLVAVARQVAVESCAHEIFVAVGCHCEPFIHFQKFFLEAVFAN 145

RESULT 3  
 US-09-949-889-3  
 ; Sequence 4, Application US/99949889  
 ; Patent No. US20020054881A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CONSILIO NAZIONALE DELLE PIERCE  
 ; TITLE OF INVENTION: VARIANTS OF ALLERGENIC PROTEINS OF THE GROUP 2 OF  
 ; FILE REFERENCE: DERMATOPHAGOIDES  
 ; CURRENT FILING DATE: 2001/09/12  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: Patent In Ver. 2.1  
 ; SEQ ID NO 4  
 ; LENGTH: 129  
 ; TYPE: PRT  
 ; ORGANISM: Dermaphagoides pteromyssinus  
 US-09-949-889-3

Query Match 94.5%; Score 653; DB 10; Length 129;  
 Best Local Similarity 94.6%; Pred. No. 5,7e-67;  
 Matches 122; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 C1 MYKILICSLVAVARQVAVESCAHEIFVAVGCHCEPFIHFQKFFLEAVFAN 61  
 DB 1 MYKILICSLVAVARQVAVESCAHEIFVAVGCHCEPFIHFQKFFLEAVFAN 61  
 C2 MYKILICSLVAVARQVAVESCAHEIFVAVGCHCEPFIHFQKFFLEAVFAN 121  
 DB 1 MYKILICSLVAVARQVAVESCAHEIFVAVGCHCEPFIHFQKFFLEAVFAN 121  
 C3 MYKILICSLVAVARQVAVESCAHEIFVAVGCHCEPFIHFQKFFLEAVFAN 145  
 DB 1 MYKILICSLVAVARQVAVESCAHEIFVAVGCHCEPFIHFQKFFLEAVFAN 145

RESULT 4  
 US-09-860-793-3  
 ; Sequence 3, Application US/99949889  
 ; Patent No. US20020136734A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: PRUETT, JOHN H  
 ; TITLE OF INVENTION: VACCINES FOR THE PROTECTION OF CATSLE FROM PNEUMOTIC  
 ; FILE REFERENCE: DOCKET 0047 96 - JOHN H. PRUETT ET AL.  
 ; CURRENT FILING DATE: 2001-05-18  
 ; NUMBER OF SEQ ID NOS: 25  
 ; SOFTWARE: Patent In Ver. 2.1  
 ; SEQ ID NO 3  
 ; LENGTH: 143  
 ; TYPE: PRT  
 ; ORGANISM: Pteromyssinus  
 US-09-860-793-3

; APPLICANT: Teuever, Kevin B  
 ; APPLICANT: Kunz, Sidney E  
 ; APPLICANT: Fisher, William F  
 ; TITLE OF INVENTION: Vaccines for the Protection of Catsle from Pteromyssinus  
 ; FILE REFERENCE: DOCKET 0047 96 - JOHN H. PRUETT ET AL.  
 ; CURRENT FILING DATE: 2001-05-18  
 ; NUMBER OF SEQ ID NOS: 25  
 ; SOFTWARE: Patent In Ver. 2.1  
 ; SEQ ID NO 3  
 ; LENGTH: 143  
 ; TYPE: PRT  
 ; ORGANISM: Pteromyssinus  
 US-09-860-793-3

Query Match 39.7%; Score 206.5; DB 10; Length 143;  
 Best Local Similarity 37.0%; Pred. No. 1.6e-27;  
 Matches 54; Conservative 42; Mismatches 46; Indels 3; Gaps 3;  
 C1 MYKILICSLVAVARQVAVESCAHEIFVAVGCHCEPFIHFQKFFLEAVFAN 61  
 DB 1 MYKILICSLVAVARQVAVESCAHEIFVAVGCHCEPFIHFQKFFLEAVFAN 61  
 C2 MYKILICSLVAVARQVAVESCAHEIFVAVGCHCEPFIHFQKFFLEAVFAN 121  
 DB 1 MYKILICSLVAVARQVAVESCAHEIFVAVGCHCEPFIHFQKFFLEAVFAN 121  
 C3 MYKILICSLVAVARQVAVESCAHEIFVAVGCHCEPFIHFQKFFLEAVFAN 143  
 DB 1 MYKILICSLVAVARQVAVESCAHEIFVAVGCHCEPFIHFQKFFLEAVFAN 143

RESULT 5  
 US-09-860-793-1  
 ; Sequence 3, Application US/99949889  
 ; Patent No. US20020136734A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: PRUETT, JOHN H  
 ; APPLICANT: Teuever, Kevin B  
 ; APPLICANT: Kunz, Sidney E  
 ; APPLICANT: Fisher, William F  
 ; TITLE OF INVENTION: Vaccines for the Protection of Catsle from Pteromyssinus  
 ; FILE REFERENCE: DOCKET 0047 96 - JOHN H. PRUETT ET AL.  
 ; CURRENT FILING DATE: 2001-05-18  
 ; NUMBER OF SEQ ID NOS: 25  
 ; SOFTWARE: Patent In Ver. 2.1  
 ; SEQ ID NO 1  
 ; LENGTH: 125  
 ; TYPE: PRT  
 ; ORGANISM: Pteromyssinus  
 ; NAME/KEY: VAPANT  
 ; LOCATION: (1)  
 ; GROUP INFORMATION: Y at position 1 may also be C or S or V  
 US-09-860-793-1

Query Match 36.7%; Score 202.5; DB 10; Length 126;  
 Best Local Similarity 38.3%; Pred. No. 5.7e-25;  
 Matches 49; Conservative 37; Mismatches 39; Indels 3; Gaps 3;  
 C1 MYKILICSLVAVARQVAVESCAHEIFVAVGCHCEPFIHFQKFFLEAVFAN 61  
 DB 1 MYKILICSLVAVARQVAVESCAHEIFVAVGCHCEPFIHFQKFFLEAVFAN 61  
 C2 MYKILICSLVAVARQVAVESCAHEIFVAVGCHCEPFIHFQKFFLEAVFAN 126  
 DB 1 MYKILICSLVAVARQVAVESCAHEIFVAVGCHCEPFIHFQKFFLEAVFAN 126  
 C3 MYKILICSLVAVARQVAVESCAHEIFVAVGCHCEPFIHFQKFFLEAVFAN 143  
 DB 1 MYKILICSLVAVARQVAVESCAHEIFVAVGCHCEPFIHFQKFFLEAVFAN 143



Db 61 QIFVETHTGCTWYFTHFFVTHFTVYTSIPATLFTTA::AFTHFFHFF::11-  
 QY 139 ALHAKRD 146  
 Db 119 VINGEIO 126

## RESULT 6

US-10-114-893 34  
 ; Sequence 34, Application US/10114893  
 ; Publication No. US2002033567A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Jacobs, Kenneth  
 ; APPLICANT: McCoy, John M.  
 ; APPLICANT: LaValle, Edward R.  
 ; APPLICANT: Collins-Racie, Lisa A.  
 ; APPLICANT: Evans, Cheryl  
 ; APPLICANT: Merberg, David  
 ; APPLICANT: Treacy, Maurice  
 ; APPLICANT: Bowman, Michael R.  
 ; APPLICANT: Spaulding, Vicki  
 ; APPLICANT: Carlini, Erika L., M.Keough  
 ; APPLICANT: Kelleher, Kerry S.  
 ; APPLICANT: Genetics Institute, Inc  
 ; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM  
 ; FILE REFERENCE: GI 6000 10A  
 ; CURRENT APPLICATION NUMBER: US/10/114,893  
 ; CURRENT FILING DATE: 2002-04-02  
 ; EARLIER APPLICATION NUMBER: 09/413,232  
 ; EARLIER FILING DATE: 1999-10-06  
 ; NUMBER OF SEQ ID NOS: 121  
 ; SOFTWARE: Patent In Ver. 2.0  
 ; SEQ ID NO 34  
 ; LENGTH: 151  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-114-893-34

Query Match 15.9%, Score 123, DB 9, Length 151;

Best Local Similarity 29.9%, Pred. No. 1 to 56;  
 Matches 35, Conservative 26, Mismatches 46, Indels 10, Gaps 57

QY 6 LLSLLVAARARQGVVWVTHANFF--HSAVVPVSTHVSFPLHHPFPHLEAVFANEN 60  
 Db 9 LLALSTAAQA-EPVGFPTDNGSVGVIVFVNVSP--PTQPLDSGSGSYNVVIFSNIQ 60  
 QY 64 TTTATFTFVASTGASIGFVVPVSTDPNATV-MATPLVKGQGVVFVTVWVFIAPKSE 119  
 Db 67 GPTATATVTHVWVGGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGVGV 119

## RESULT 7

US-09-925-302-529  
 ; Sequence 529, Application US/09092502  
 ; Patent No. US200203044941A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al.  
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
 ; FILE REFERENCE: PA104  
 ; CURRENT APPLICATION NUMBER: US/09/925,302  
 ; PRIOR APPLICATION NUMBER: PCT/US00/05919  
 ; PRIOR FILING DATE: 2000-03-08  
 ; PRIOR APPLICATION NUMBER: 60/124,270  
 ; PRIOR FILING DATE: 1999-03-12  
 ; NUMBER OF SEQ ID NOS: 347  
 ; SOFTWARE: Patent In Ver. 2.0  
 ; SEQ ID NO 529  
 ; LENGTH: 179  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-925-302-529

Query Match 15.9%, Score 123, DB 10, Length 179;  
 Best Local Similarity 29.9%, Pred. No. 1 to 66;  
 Matches 35, Conservative 26, Mismatches 46, Indels 10, Gaps 57

QY 6 LLSLLVAARARQGVVWVTHANFF--HSAVVPVSTHVSFPLHHPFPHLEAVFANEN 63  
 Db 37 LLALSTAAQA-EPVGFPTDNGSVGVIVFVNVSP--PTQPLDSGSGSYNVVIFSNIQ 94  
 QY 64 TTTATFTFVASTGASIGFVVPVSTDPNATV-MATPLVKGQGVVFVTVWVFIAPKSE 119  
 Db 95 SRSKAAVNHGILMVGVPFPIPERPISLSSNVLPLKATVY--INPLVPEE 146

## RESULT 8

US-09-925-302-854  
 ; Sequence 854, Application US/09925302  
 ; Patent No. US20030044941A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al.  
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
 ; FILE REFERENCE: PA104  
 ; CURRENT APPLICATION NUMBER: US/09/925,302  
 ; CURRENT FILING DATE: 2001-08-10  
 ; PRIOR APPLICATION NUMBER: PCT/US00/05918  
 ; PRIOR FILING DATE: 2000-03-08  
 ; PRIOR APPLICATION NUMBER: 60/104,270  
 ; PRIOR FILING DATE: 1999-03-12  
 ; NUMBER OF SEQ ID NOS: 896  
 ; SOFTWARE: Patent In Ver. 2.0  
 ; SEQ ID NO 854  
 ; LENGTH: 130  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: SITE  
 ; LOCATION: (66)  
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L amino acids  
 ; NAME/KEY: SITE  
 ; LOCATION: (70)  
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L amino acids  
 ; NAME/KEY: SITE  
 ; LOCATION: (73)  
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L amino acids  
 ; NAME/KEY: SITE  
 ; LOCATION: (118)  
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L amino acids  
 ; NAME/KEY: SITE  
 ; LOCATION: (128)  
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L amino acids  
 ; NAME/KEY: SITE  
 ; LOCATION: (129)  
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L amino acids  
 ; NAME/KEY: SITE  
 ; LOCATION: (130)  
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L amino acids  
 US-09-925-302-854

Query Match 15.5%, Score 120, DB 10, Length 130;

Best Local Similarity 29.9%, Pred. No. 2,46-05;  
 Matches 35, Conservative 23, Mismatches 49, Indels 10, Gaps 57

QY 6 LLSLLVAARARQGVVWVTHANFF--HSAVVPVSTHVSFPLHHPFPHLEAVFANEN 93  
 Db 12 LLALSTAAQA-EPVGFPTDNGSVGVIVFVNVSP--PTQPLDSGSGSYNVVIFSNIQ 69  
 QY 64 TTTATFTFVASTGASIGFVVPVSTDPNATV-MATPLVKGQGVVFVTVWVFIAPKSE 119  
 Db 70 ALPAPAVNHGILMVGVPFPIPERPISLSSNVLPLKATVY--INPLVPEE 121

## RESULT 9

US-10-114-893-168  
 ; Sequence 168, Application US/10114893

```

: Publication No. US20020193562A1
: GENERAL INFORMATION:
: APPLICANT: Jacobs, Kenneth
: APPLICANT: McCoy, John M.
: APPLICANT: LaValle, Edward P.
: APPLICANT: Collins-Racie, Lisa A.
: APPLICANT: Evans, Cheryl
: APPLICANT: Merberg, David
: APPLICANT: Treacy, Maurice
: APPLICANT: Bowman, Michael R.
: APPLICANT: Spaulding, Vikki
: APPLICANT: Carlin-Duckett, McKeough
: APPLICANT: Kelleher, Kerry S.
: APPLICANT: Genetics Institute, Inc.
: TITLE OF INVENTION: SCRIPTED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
: FILE REFERENCE: GI 6000-10A
: CURRENT APPLICATION NUMBER: US/10/114,803
: CURRENT FILING DATE: 2002-04-02
: EARLIER APPLICATION NUMBER: 09/413,232
: EARLIER FILING DATE: 1999-10-06
: NUMBER OF SEQ ID NOS: 321
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 168
: LENGTH: 149
: TYPE: PRT
: ORGANISM: Mus musculus
: FEATURE:
: NAME/KEY: UNSURE
: LOCATION: (95)
: us-10-114-803-168

Query Match 15.5% Score 119.5; DB 9; Length 149;
Best Local Similarity 26.4% P=1.3e-36;
Matches 34; Conservative 30; Mismatches 55; Indels 13; Gaps 5;

QY 4 CIGITLVAAAPDVVDFQCANH---EIKVVLVPGCHGSEPTIIEGKPPQLKAVPEANCN 53
DB 8 ILLALVAASQAEPLHFDGSKGVKIVNVVSPC-PTDSCQLHKQGSYSVAITTSQTQ 66
QY 64 TKTAKIFKASIDLEVDVPGCIDNACHY-MKCPVLVGGQYDIKYTWVFKAPKSE--- 119
DB 67 SQNTALVHGILGIPVFPPEIPEDGGYGNINETIQDKYSY.....INKLVNREVS 121
QY 120 -NVVTVVWMT 130
DB 122 IKLVVWKLDD 133

RESULT 10
US-10-040-916-45
: Sequence 45 Application US/09-860-793
: Patent No. US20020193562A1
: GENERAL INFORMATION:
: APPLICANT: Jacobs, Kenneth
: APPLICANT: McCoy, John
: APPLICANT: LaValle, Edward
: APPLICANT: Racie, Lisa
: APPLICANT: Merberg, David
: APPLICANT: Treacy, Maurice
: APPLICANT: Evans, Cheryl
: APPLICANT: Spaulding, Vikki
: TITLE OF INVENTION: SCRIPTED PROTEINS AND POLYNUCLEOTIDES
: NUMBER OF SEQUENCES: 71
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genetics Institute, Inc.
: STREET: 47 Cambridgepark Drive
: CITY: Cambridge
: STATE: Massachusetts
: COUNTRY: U.S.A.
: ZIP: 02140
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk

```

```

: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/10/040,916
: FILING DATE: 07 Jan 2002
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/837,029
: FILING DATE: 07-FEB-1997
: APPLICATION NUMBER: 08/686,878
: FILING DATE: <Unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: Brown, Scott A.
: REGISTRATION NUMBER: 32,724
: TELEPHONE: (617) 498-8224
: TELEFAX: (617) 876-5851
: INFORMATION FOR SEQ ID NO: 45:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 130 amino acids
: TYPE: amino acid
: STRANDEDNESS: <Unknown>
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-10-040-916-45

Query Match 14.0% Score 108.5; DB 12; Length 120;
Best Local Similarity 26.4% P=4.9e-05;
Matches 31; Conservative 26; Mismatches 51; Indels 9; Gaps 5;

QY 5 LCLSLVAAVAGQVGVETCAH--EIHVYVGHGSEPTIIEGKPPQLKAVPEANCN 61
DB 8 ILLALVAASQAEPLHFDGSKGVKIVNVVSPC-PTDSCQLHKQGSYSVAITTSQTQ 66
QY 64 TKTAKIFKASIDLEVDVPGCIDNACHY-MKCPVLVGGQYDIKYTWVFKAPKSE 119
DB 67 SQNTALVHGILGIPVFPPEIPEDGGYGNINETIQDKYSY.....INKLVNREVS 118

RESULT 11
US-09-860-793-7
: Sequence 7 Application US/09-860-793
: Patent No. US20020193562A1
: GENERAL INFORMATION:
: APPLICANT: Pruett, John H.
: APPLICANT: Temeyer, Kevin B.
: APPLICANT: Kunz, Sidney E.
: APPLICANT: Fisher, William F.
: TITLE OF INVENTION: Vaccines for the Prevention of Cancer from Peptidic
: TITLE REFERENCE: Docket 004/96; John H. Pruett et al.
: CURRENT APPLICATION NUMBER: US/09/860,793
: CURRENT FILING DATE: 2001-05-18
: PRIOR APPLICATION NUMBER: 09/366,603
: PRIOR FILING DATE: 1999-08-03
: NUMBER OF SEQ ID NOS: 25
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 7
: LENGTH: 22
: TYPE: PRT
: ORGANISM: Dermatophagoides farinae
: US-09-860-793-7

Query Match 13.8% Score 107; DB 10; Length 22;
Best Local Similarity 26.4% P=7.1e-06;
Matches 19; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 19 QVIVKDCANHEIKVLPQCHG 40
DB 1 QVTVKDCANHEIKVLPQCHG 22

```







QY 1 MWYFLLCLSLVAAPVQVPCANREIKYVLPQCHSGSEPCIIHSPFFPLEAVPEA 60  
 DB 1 MWYFLLCLSLVAAPVQVPCANREIKYVLPQCHSGSEPCIIHSPFFPLEAVPEA 60  
 QY 61 NONTPTAFIFPASTGVLEVPQIDFNACHVWVPCFVWQCCQVQVYVWVNDVIAAPCPN 100  
 DB 61 NONTPTAFIFPASTGVLEVPQIDFNACHVWVPCFVWQCCQVQVYVWVNDVIAAPCPN 100  
 QY 121 VVTVKMGSDGVLAIAATHAIPD 146  
 DB 121 VVTVKMGSDGVLAIAATHAIPD 146

RESULT 2  
 US-08-461-809-4  
 : Sequence 4, Application US/08/461-809-4  
 : Patent No. 5770202  
 : GENERAL INFORMATION:  
 : APPLICANT:  
 : TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLELGENS FROM  
 : NUMBER OF SEQUENCES: 13  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: LAHIVE & COCKFIELD  
 : STREET: 60 STATE STREET, SUITE 510  
 : CITY: BOSTON  
 : STATE: MA  
 : COUNTRY: USA  
 : ZIP: 02109  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: ASCII TEXT  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/461-809-4  
 : FILING DATE:  
 : CLASSIFICATION: 424  
 : PRIOR APPLICATION NUMBER: US 07/945,288  
 : FILING DATE: 10 SEPTEMBER 1990  
 : APPLICATION NUMBER: US 580,655  
 : FILING DATE: 11 SEPTEMBER 1990  
 : APPLICATION NUMBER: US 458,642  
 : FILING DATE: 13 FEBRUARY 1990  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: MANDRAGOURAS, AMY E.  
 : REGISTRATION NUMBER: 36,207  
 : REFERENCE/POCKET NUMBER: IPC 0100C (INT 024)  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: (617) 227-7400  
 : TELEFAX: (617) 227-5941  
 : INFORMATION FOR SEQ ID NO: 4:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 146 amino acids  
 : TYPE: amino acid  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: Protein  
 : US-08-461-809-4

Query Match 100.0%; Score 773; DB 1; Length 146;  
 Best Local Similarity 100.0%; Pred. No. 7.3e-89;  
 Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MWYFLLCLSLVAAPVQVPCANREIKYVLPQCHSGSEPCIIHSPFFPLEAVPEA 60  
 DB 1 MWYFLLCLSLVAAPVQVPCANREIKYVLPQCHSGSEPCIIHSPFFPLEAVPEA 60  
 QY 61 NONTPTAFIFPASTGVLEVPQIDFNACHVWVPCFVWQCCQVQVYVWVNDVIAAPCPN 100  
 DB 61 NONTPTAFIFPASTGVLEVPQIDFNACHVWVPCFVWQCCQVQVYVWVNDVIAAPCPN 100  
 QY 121 VVTVKMGSDGVLAIAATHAIPD 146

DB 121 VVTVKMGSDGVLAIAATHAIPD 146  
 RESULT 3  
 US-08-461-809-4  
 : Sequence 4, Application US/08/461-809-4  
 : Patent No. 5770202  
 : GENERAL INFORMATION:  
 : APPLICANT:  
 : TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLELGENS FROM  
 : NUMBER OF SEQUENCES: 13  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: LAHIVE & COCKFIELD  
 : STREET: 60 STATE STREET, SUITE 510  
 : CITY: BOSTON  
 : STATE: MA  
 : COUNTRY: USA  
 : ZIP: 02109  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: ASCII TEXT  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/461-809-4  
 : FILING DATE:  
 : CLASSIFICATION: 424  
 : PRIOR APPLICATION NUMBER: US 07/945,288  
 : FILING DATE: 10 SEPTEMBER 1990  
 : APPLICATION NUMBER: US 580,655  
 : FILING DATE: 11 SEPTEMBER 1990  
 : APPLICATION NUMBER: US 458,642  
 : FILING DATE: 13 FEBRUARY 1990  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: MANDRAGOURAS, AMY E.  
 : REGISTRATION NUMBER: 36,207  
 : REFERENCE/POCKET NUMBER: IPC 0100C (INT 024)  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: (617) 227-7400  
 : TELEFAX: (617) 227-5941  
 : INFORMATION FOR SEQ ID NO: 4:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 146 amino acids  
 : TYPE: amino acid  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: Protein  
 : US-08-461-809-4

Query Match 100.0%; Score 773; DB 1; Length 146;  
 Best Local Similarity 100.0%; Pred. No. 7.3e-89;  
 Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MWYFLLCLSLVAAPVQVPCANREIKYVLPQCHSGSEPCIIHSPFFPLEAVPEA 60  
 DB 1 MWYFLLCLSLVAAPVQVPCANREIKYVLPQCHSGSEPCIIHSPFFPLEAVPEA 60  
 QY 61 NONTPTAFIFPASTGVLEVPQIDFNACHVWVPCFVWQCCQVQVYVWVNDVIAAPCPN 120  
 DB 61 NONTPTAFIFPASTGVLEVPQIDFNACHVWVPCFVWQCCQVQVYVWVNDVIAAPCPN 120  
 QY 121 VVTVKMGSDGVLAIAATHAIPD 146  
 DB 121 VVTVKMGSDGVLAIAATHAIPD 146  
 RESULT 4  
 US-08-461-441-4  
 : Sequence 4, Application US/08/461-441-4  
 : Patent No. 5770002  
 : GENERAL INFORMATION:



STATE: MA  
COUNTRY: USA  
ZIP: 02154  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII TEXT  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: 08/444,307  
FILING DATE: 07 June 1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/444,307  
FILING DATE: 07 June 1995  
NAME: CRAIG, ANNE I.  
REGISTRATION NUMBER: 32,976  
REPRESENTATIVE NUMBER: 017 605  
TELEPHONE: (617) 466-6000  
TELEFAX: (617) 466-6040  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 146 amino acids  
TYPE: amine acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-484-296-4

Query Match 100.0% Score 773; DP 2; Length 146.

Best Local Similarity 100.0% Prod No. 7 3e-88;

Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY : MNYPTTCTTAAVAPDGVVDTANSHETTPVVTGTHSEFFTHPQVFEQPAVPEA 60  
DB : MNYPTTCTTAAVAPDGVVDTANSHETTPVVTGTHSEFFTHPQVFEQPAVPEA 60  
C : MNYPTTCTTAAVAPDGVVDTANSHETTPVVTGTHSEFFTHPQVFEQPAVPEA 60  
DE : MNYPTTCTTAAVAPDGVVDTANSHETTPVVTGTHSEFFTHPQVFEQPAVPEA 60  
QY : MNYPTTCTTAAVAPDGVVDTANSHETTPVVTGTHSEFFTHPQVFEQPAVPEA 60  
DB : MNYPTTCTTAAVAPDGVVDTANSHETTPVVTGTHSEFFTHPQVFEQPAVPEA 60  
C : MNYPTTCTTAAVAPDGVVDTANSHETTPVVTGTHSEFFTHPQVFEQPAVPEA 60  
DE : MNYPTTCTTAAVAPDGVVDTANSHETTPVVTGTHSEFFTHPQVFEQPAVPEA 60

RESULT 7  
US-08-484-296-4  
Sequence 4, Application US/08444296  
Patent No. 6268491  
GENERAL INFORMATION:  
APPLICANT: Garman, Richard  
APPLICANT: Greenstein, Julia  
APPLICANT: Kuo, Mei Shue  
APPLICANT: Rogers, Bruce  
APPLICANT: Frances, Henry  
APPLICANT: Chen, Xian  
APPLICANT: Evans, Sean  
APPLICANT: Shaked, Zeev  
TITLE OF INVENTION: CELL EFFICES OF THE MAJOR ALLERGENS  
TITLE OF INVENTION: FROM DERMATOPHAGOIDES (HOUSE DUST MITE)  
NUMBER OF SEQUENCES: 107  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMUNOLOGIC PHARMACEUTICAL CORPORATION  
STREET: 610 LINCOLN STREET  
CITY: WALTHAM  
STATE: MA  
COUNTRY: USA  
ZIP: 02154  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII TEXT  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: 08/444,307  
FILING DATE: 07 June 1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/444,307  
FILING DATE: 07 June 1995  
NAME: MANDAGOURAS, AMY E.  
REGISTRATION NUMBER: 32,976  
REFERENCE/DOCKET NUMBER: IPC-0100C (IMI-024)  
TELECOMMUNICATION INFORMATION:

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII TEXT  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: 08/444,307  
FILING DATE: 07 June 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/444,307  
FILING DATE: 07 June 1995  
NAME: CRAIG, ANNE I.  
REGISTRATION NUMBER: 32,976  
REPRESENTATIVE NUMBER: 017 605  
TELEPHONE: (617) 466-6000  
TELEFAX: (617) 466-6040  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 146 amino acids  
TYPE: amine acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-484-296-4

Query Match 100.0% Score 773; DP 2; Length 146.

Best Local Similarity 100.0% Prod No. 7 3e-88;

Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY : MNYPTTCTTAAVAPDGVVDTANSHETTPVVTGTHSEFFTHPQVFEQPAVPEA 60  
DB : MNYPTTCTTAAVAPDGVVDTANSHETTPVVTGTHSEFFTHPQVFEQPAVPEA 60  
C : MNYPTTCTTAAVAPDGVVDTANSHETTPVVTGTHSEFFTHPQVFEQPAVPEA 60  
DE : MNYPTTCTTAAVAPDGVVDTANSHETTPVVTGTHSEFFTHPQVFEQPAVPEA 60  
QY : MNYPTTCTTAAVAPDGVVDTANSHETTPVVTGTHSEFFTHPQVFEQPAVPEA 60  
DB : MNYPTTCTTAAVAPDGVVDTANSHETTPVVTGTHSEFFTHPQVFEQPAVPEA 60  
C : MNYPTTCTTAAVAPDGVVDTANSHETTPVVTGTHSEFFTHPQVFEQPAVPEA 60  
DE : MNYPTTCTTAAVAPDGVVDTANSHETTPVVTGTHSEFFTHPQVFEQPAVPEA 60

RESULT 8  
US-08-484-296-4  
Sequence 4, Application PC/TUS9308518  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: CELL EFFICES OF THE MAJOR ALLERGENS FROM  
TITLE OF INVENTION: DERMATOPHAGOIDES  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 STATE STREET, SUITE 510  
CITY: BOSTON  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII TEXT  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: 08/444,307  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/444,307  
FILING DATE: 10 SEPTEMBER 1992  
NAME: MANDAGOURAS, AMY E.  
REGISTRATION NUMBER: 32,976  
REFERENCE/DOCKET NUMBER: IPC-0100C (IMI-024)  
TELECOMMUNICATION INFORMATION:







```

;
; NAME/KEY: misc feature
; LOCATION: 114
; OTHER INFORMATION: /label-Xaa is Asp or Asn
;
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 127
; OTHER INFORMATION: /label-Xaa is Ile or Leu
; US-06-461 803-12

```

|                       |              |                    |               |             |
|-----------------------|--------------|--------------------|---------------|-------------|
| Query Match           | 87.5%        | Score 676;         | DB 1;         | Length 129; |
| Best local Similarity | 97.7%        | Pred. No. 6.1e-76; |               |             |
| Matches 126;          | Conservative | 0;                 | Mismatches 3; | Indels 0;   |
| Gaps                  | 0;           |                    |               |             |

|    |     |                                                              |
|----|-----|--------------------------------------------------------------|
| 04 | 18  | DOVVVFATRIEIEFVVFVTHSEETIEHFHFIEHSAVFAANFYTAETAFIEASING 79   |
| 05 | 19  |                                                              |
| 06 | 1   | DOVVVFANHFVKVTVPGHUSEETIEHFHFIEHSAVFAANFYTAETAFIEASING 60    |
| 07 | 2   |                                                              |
| 08 | 78  | LEVNVGIDPNACHYMCPLVKGQOVDIVTVWNVKTIAPKSENVTVTVPMGGCGYLAC 137 |
| 09 | 79  |                                                              |
| 0A | 61  | LEVNVGIDPNACHYMCPLVKGQOVDIVTVWNVKTIAPKSENVTVTVPMGGCGYLAC 129 |
| 0B | 62  |                                                              |
| 0C | 118 | IATHAKIRD 146                                                |
| 0D | 119 |                                                              |
| 0E | 121 | IATHAKIRD 129                                                |
| 0F | 122 |                                                              |

```

RESULT 13
US:09-461-441-12
: Sequence 12, Application US:08461441
: Patent No. 5773002
: GENERAL INFORMATION:
: APPLICANT.
: TITLE OF INVENTION: 1 CELL LINES OF THE MARCH ALLERGIES FROM
: TITLE OF INVENTION: DERMATOPHAGOIDES

```

```

, NAME/KEY: misc feature
, LOCATION: 47
, OTHER INFORMATION: /label-xaa is Thr or Ser
, FEATURE:
, NAME/KEY: misc feature
, LOCATION: 114
, OTHER INFORMATION: /label-xaa is Asp or Asn
, FEATURE:
, NAME/KEY: misc feature
, LOCATION: 127
, OTHER INFORMATION: /label-xaa is Ile or Leu
US 08 461 441-12

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|                       |              |                  |               |             |
|-----------------------|--------------|------------------|---------------|-------------|
| Query Match           | 97.5%        | Score 676;       | DB 1;         | Length 129; |
| Best Local Similarity | 97.7%        | Ref. No. 6.1976; |               |             |
| Matches 126;          | Conservative | 0;               | Mismatches 3; | Indels 0;   |
|                       |              |                  |               | Gaps 0;     |

[illegible]

RESULT 14  
PCT-US93-08518-12  
Sequence 12, Application PCTUS93-08518  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: CELL EFFLUX OF THE MAJOR ANTICANCER FROM  
DERMATOPHAGOIDES

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1 OTHER INFORMATION: /label Xaa is Thr or Ser
2 FEATURE:
3 NAME/KEY: misc feature
4 LOCATION: 114
5 OTHER INFORMATION: /label Xaa is Asp or Asn
6 FEATURE:
7 NAME/KEY: misc feature
8 LOCATION: 123
9 OTHER INFORMATION: /label Xaa is Ile or Leu
10 PCT-US93/091471
11
12 (Seq. Var. 1) 114 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150
13 Best Local Similarity 97.74; Pred. No. 6 (1e-06);
14 Matches 101, Conservative 9, Mismatches 1, Indels 0, Gaps 0
15
16 QY 19 114 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150
17 Db 1 114 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150
18 QY 76 114 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150
19 Db 1 114 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150
20 QY 138 IATHAKIRD 146
21 Db 121 IATHAKIRD 129

```

## RESULT 15

```

US-08-888-888-4
1 Sequence 4, Application US/09288989
2 Patent No. 5798099
3 GENERAL INFORMATION:
4 APPLICANT: YUUKI, Toshifumi
5 APPLICANT: OKUMURA, Yasushi
6 APPLICANT: YAMAKAWA, Hiroshi
7 TITLE OF INVENTION: DNA ENCODING A MAJOR MITE ALLERGEN AND
8 TITLE OF INVENTION: THE USE THEREOF
9 NUMBER OF SEQUENCES: 4
10 CORRESPONDENCE ADDRESS:
11 ADDRESSEE: BROWDY AND NEIMARK
12 STREET: 419 SEVENTH ST., N.W., SUITE 300
13 CITY: WASHINGTON
14 STATE: DC
15 COUNTRY: USA
16 ZIP: 20004
17 COMPUTER READABLE FORM:
18 MEDIUM TYPE: Floppy disk
19 Computer: IBM PC compatible
20 OPERATING SYSTEM: PC-DOS/MS-DOS
21 SOFTWARE: Patent In Release #1 0, Version #1 25
22 CURRENT APPLICATION DATA:
23 APPLICATION NUMBER: US/98/288,988
24 FILING DATE:
25 CLASSIFICATION: 435
26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER: 07/659,596
28 FILING DATE: 21-FEB-1991
29 ATTORNEY/AGENT INFORMATION:
30 NAME: Cooper, Liver P
31 REGISTRATION NUMBER: 39,085
32 REFERENCE/DOCKET NUMBER: YUUKI1
33 TELECOMMUNICATION INFORMATION:
34 TELEPHONE: 202-638-5197
35 TELEFAX: 202-737-3528
36 TELEX: 248633
37 INFORMATION FOR SEQ ID NO: 4:
38 SEQUENCE CHARACTERISTICS:
39 LENGTH: 142 amino acids
40 TYPE: amino acid
41 TOPOLOGY: linear
42 MOLECULE TYPE: protein
43 US 08 288-888-4

```

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Query Match 85.0%; Score 657; DB 1; Length 142;
Post-1:ral similarity 97.74; Pred No 6 (1e-06);
Matches 101, Conservative 12, Mismatches 6, Indels 0, Gaps 0;
QY 2 114 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150
Db 4 114 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150
QY 18 114 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150
Db 1 114 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150
QY 109 MTRCQATACATATHAKIRD 146
Db 104 MTRCQATACATATHAKIRD 140
Search completed: March 10, 2003, 13:27:04
Total time: 23.2642 secs

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GenCite version 1.4.10.4  
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QM protein protein search, using sw model

Run on: March 11, 2003, 15:23:44, Search time 18.552 Seconds  
(without alignment)  
326.161 Million cell updates/sec

Title: us-09-877-160.3

Perfect score: 773

Sequence: 1 MMVKILTSIAVAARVGV.....VMSSGVLAIAIAHAIKD 146

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 112992 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112992

Minimum DB seq length: 0

Maximum DB seq length: 2600000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt\_43.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 773   | 100         | 0      | 1     | ALL2 DERPPT |
| 2          | 687   | 88.9        | 146    | 1     | ALL2 DERPPT |
| 3          | 676   | 87.5        | 145    | 1     | ALL2 DERPPT |
| 4          | 290.5 | 37.6        | 141    | 1     | ALL2 DERPPT |
| 5          | 278.5 | 36.0        | 141    | 1     | ALL2 DERPPT |
| 6          | 135.5 | 17.5        | 149    | 1     | NP22 DERPPT |
| 7          | 127.5 | 16.5        | 149    | 1     | NP22 DERPPT |
| 8          | 126.5 | 16.4        | 148    | 1     | NP22 DERPPT |
| 9          | 123   | 15.9        | 151    | 1     | NP22 DERPPT |
| 10         | 118.5 | 15.3        | 149    | 1     | NP22 DERPPT |
| 11         | 112   | 14.5        | 149    | 1     | NP22 DERPPT |
| 12         | 105   | 13.6        | 149    | 1     | NP22 DERPPT |
| 13         | 90.5  | 11.7        | 145    | 1     | ES16 DERPPT |
| 14         | 89    | 11.5        | 151    | 1     | YG27 DERPPT |
| 15         | 86.5  | 11.2        | 577    | 1     | ITB6 DERPPT |
| 16         | 79.5  | 10.3        | 788    | 1     | ITB6 DERPPT |
| 17         | 79    | 10.2        | 255    | 1     | ITB6 DERPPT |
| 18         | 76    | 9.8         | 175    | 1     | DEST DERPPT |
| 19         | 74.5  | 9.6         | 324    | 1     | CAV1 DERPPT |
| 20         | 73.5  | 9.5         | 2109   | 1     | PGCA DERPPT |
| 21         | 73    | 9.4         | 2531   | 1     | ITB6 DERPPT |
| 22         | 72.5  | 9.4         | 309    | 1     | ITB6 DERPPT |
| 23         | 72.5  | 9.4         | 423    | 1     | ITB6 DERPPT |
| 24         | 72    | 9.3         | 213    | 1     | ITB6 DERPPT |
| 25         | 72    | 9.3         | 381    | 1     | ITB6 DERPPT |
| 26         | 71    | 9.2         | 183    | 1     | ITB6 DERPPT |
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| 28         | 70.5  | 9.1         | 183    | 1     | ITB6 DERPPT |
| 29         | 70.5  | 9.1         | 310    | 1     | ITB6 DERPPT |
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| 31         | 70.5  | 9.1         | 787    | 1     | ITB6 DERPPT |
| 32         | 70    | 9.1         | 160    | 1     | ITB6 DERPPT |
| 33         | 70    | 9.1         | 351    | 1     | ITB6 DERPPT |

34 70 9.1 593 1 SUMT YEAST  
35 69.5 9.0 1245 1 F022 STGCC  
36 69 8.8 459 1 P024 HUMAN  
37 68 8.8 705 1 DPO2 YEAST  
38 67.5 8.7 310 1 MTA2 STPRN  
39 67.5 8.7 631 1 IF2 MICON  
40 67 8.7 227 1 IF2 MESAU  
41 67 8.7 983 1 CAGE HELPF  
42 67 8.7 983 1 CAGE HELPF  
43 67 8.7 1460 1 M150 YEAST  
44 66.5 8.6 310 1 MTA2 STGCC  
45 66.5 8.6 936 1 EAE CITFR

#### ALIGNMENTS

RESULT 1  
ALL2 DERPPT  
ID ALL2 DERPPT STANDARD; PRT; 146 AA.  
AC P49278,  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Mite Group 2 allergen Der p 2 precursor (Der p II) (DPX).  
GN DERP2.  
CC Dermatophagoides pteronyssinus (House-dust mite).  
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;  
OC Acariformes; Sarcoptiformes; Astigmata; Analgoidea; Pyroglyphidae;  
OC Dermatophagoides.  
OX NCBI\_TaxID=6956;  
RN [1]  
PP SEQUENCE FROM N.A.  
FX MEDLINE:3255201, PubMed 3341191;  
RA Chua K Y, Doyle C P, Simpson R J, Turner K J, Stewart G A,  
RA Thomas W R.;  
RT "Isolation of cDNA coding for the major mite allergen Der p II by IgE  
RT plaque immunosay.",  
EL Int. Arch. Allergy Appl. Immunol. 93:115-122(1990).  
RN [2]  
PP SEQUENCE FROM N.A. AND VARIANTS.  
FX MEDLINE:2129932, PubMed 1199675;  
RA Smith W A, Hales B J, Jarnicki A G, Thomas W R.;  
RT "Allergens of wild house dust mites, environmental Der p 1 and Der p 2  
RT sequence polymorphisms.",  
FX J. Allergy Clin. Immunol. 107:988-992(2001).  
RN [3]  
PP PARTIAL SEQUENCE OF 18-57.  
FX MEDLINE:8927984, PubMed 233406;  
RA Heymann P W, Chipman M P, Asifore P C, Fox J W.,  
RA Platts-Mills T A.;  
RT "Antigenic and structural analysis of group II allergens (Der p II  
RT and Der p II) from house dust mites (Dermatophagoides spp).",  
FX J. Allergy Clin. Immunol. 93:1055-1067(1995).  
RN [4]  
PP STRUCTURE BY NMR.  
FX MEDLINE:9840942, PubMed 977947,  
RA Mueller G A, Benjamin D C, Rule G S.;  
RT "Tertiary structure of the major house dust mite allergen Der p 2:  
RT sequential and structural homologies.",  
PL Biochemistry 31:12737-12744(1998).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC !- SIMILARITY BELONGS TO THE NPC2 FAMILY.  
CC This SWISS PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL European  
CC the European Bioinformatics Institute. There are no restrictions on its  
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CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
CC EMBL: AF262239; AAF64621; ..





[illegible]











DE SMART; SMG00001; EGF like; 1.  
 DR SMART; SMG0197; INS; 1.  
 ER PEGSITE; P300-43; INTEGRIN BETA; 1.  
 ET PEGSITE; P300-43; INTEGRIN BETA; 1.  
 FF PEGSITE; P300-43; EGF 1; TRANS; 2.  
 GG PEGSITE; P300-43; EGF 1; TRANS; 1.  
 HW Integrin; Cell adhesion; Receptor; Transmembrane; Glycoprotein;

KW Repeat.

|        |     |
|--------|-----|
| I.     | 360 |
| REPEAT |     |
| II.    | 402 |
| REPEAT |     |
| III.   | 441 |
| REPEAT |     |
| IV.    | 479 |
| REPEAT |     |

|          |     |                |
|----------|-----|----------------|
| DISULFID | 131 | BY SIMILARITY. |
| FT       | 233 | BY SIMILARITY. |
| DISULFID | 265 | BY SIMILARITY. |
| DISULFID | 265 | BY SIMILARITY. |
| DISULFID | 311 | BY SIMILARITY. |
| DISULFID | 315 | BY SIMILARITY. |
| DISULFID | 345 | BY SIMILARITY. |
| DISULFID | 335 | BY SIMILARITY. |
| DISULFID | 370 | BY SIMILARITY. |
| DISULFID | 409 | BY SIMILARITY. |

|    |          |     |     |                |
|----|----------|-----|-----|----------------|
| FT | DISULFID | 376 | 381 | BY SIMILARITY. |
| FT | DISULFID | 378 | 411 | BY SIMILARITY. |
| FT | DISULFID | 383 | 396 | BY SIMILARITY. |
| FT | DISULFID | 398 | 403 | BY SIMILARITY. |

|    |          |     |     |                |
|----|----------|-----|-----|----------------|
| FT | DISULFID | 417 | 422 | BY SIMILARITY. |
| FT | DISULFID | 419 | 450 | BY SIMILARITY. |
| FT | DISULFID | 424 | 433 | BY SIMILARITY. |
| FT | DISULFID | 435 | 442 | BY SIMILARITY. |

|    |          |     |     |                |
|----|----------|-----|-----|----------------|
| FT | DISULFID | 456 | 461 | BY SIMILARITY. |
| FT | DISULFID | 504 | 504 | BY SIMILARITY. |
| FT | DISULFID | 463 | 473 | BY SIMILARITY. |
| FT | DISULFID | 470 | 473 | BY SIMILARITY. |

|    |     |                                    |  |
|----|-----|------------------------------------|--|
| FT | 489 | BY SIMILARITY.                     |  |
| FT | 508 | BY SIMILARITY.                     |  |
| FT | 119 | N-LINKED (GLCNAC. . .) (POTENTIAL) |  |

|    |          |     |         |           |             |
|----|----------|-----|---------|-----------|-------------|
| FT | CARBOHYD | 295 | N-ALKYL | (GLUCAC.) | (POTENTIAL) |
| FT | CARBOHYD | 277 | N-ALKYL | (GLUCAC.) | (POTENTIAL) |
| FT | CARBOHYD | 322 | N-ALKYL | (GLUCAC.) | (POTENTIAL) |

|    |          |     |          |               |             |
|----|----------|-----|----------|---------------|-------------|
| FT | CARBOHYD | 455 | N-LINKED | (GLENAC. . .) | (POTENTIAL) |
| FT | CARBOHYD | 434 | N-LINKED | (GLENAC. . .) | (POTENTIAL) |
| FT | CARBOHYD | 555 | N-LINKED | (GLENAC. . .) | (POTENTIAL) |

Seq: SEQID=976; Length: 577 AA; MW: 80364 Da; pI: 5.764;  
Query Match: 11.2%; Score 90.5; DB 1; Length: 577;

Matches 29; Conservative 29; Mismatches 55; Indels 13;

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184 221FANTGE_VEL-----FANTFIP-----GATVCHARTSNTLGLICATFIPFSE
 63 22FANTFTEFVVF61000A-----HMPF1104 221010000000000000000000

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107 125 VIEWED 139

108 136 1PVZGTEFGLSESAVDHETSCPHVYLMPPZETAEPN76LIMREPLERVA

25 296 PVCLD 301

Job time : 20.5552 sec

1































RL Biochim. Biophys. Acta 591:161-164 (1979)  
 [4] SEQUENCE OF 287-348 FROM N.A.  
 PP MESLINE-9509779, PubMed:3494797;  
 RA McKee R A., Adams S., Matthews J A., Smith C.J., Smith H.;  
 RT "Molecular cloning of two cysteine proteinases from papaya  
 papaya";  
 RL Biochem. J. 237:103-110 (1986).  
 RN [5]  
 PP CATALYTIC SPECIFICITY  
 RA MESLINE-96127429, PubMed:3494797;  
 RA Buttle D.J., Richards A., Pearl L.H., Turk V., Barrett A J.,  
 RT "Selective cleavage of glycyI bonds by papaya proteinase IV",  
 PL FEBS Lett. 252:135-137 (1989).  
 RN [6]  
 RP X RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).  
 PX MESLINE-96094178, PubMed:7648992;  
 RA O'Hara B.P., Hemmings A.M., Buttle D.J., Pearl L.H.;  
 RT "Crystal structure of glycyI endopeptidase from Carica papaya: a  
 cysteine endopeptidase of unusual substrate specificity";  
 RL Biochemistry 34:13190-13195 (1995).  
 CC -1- FUNCTION: THIOL PROTEASE WITH A SUBSTRATE SPECIFICITY VERY  
 DIFFERENT FROM THE OTHER THIOL PROTEASES.  
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Gly-I-Xaa, in proteins  
 and in small molecule substrates.  
 CC -1- ENZYME REGULATION: NOT INHIBITED BY CYSTATIN.  
 CC -1- MISCELLANEOUS: SUBSTITUTION OF THE CONSERVED GLY 155 RESIDUE BY  
 GLU COULD POSSIBLY EXPLAIN THE UNUSUAL SPECIFICITY.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
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 or send an email to [license@sib.ch](mailto:license@sib.ch)).  
 CC  
 DR EMBL; X78056; CAA54974.1; -;  
 DR EMBL; X03970; CAA27608.1; -;  
 DR PIR; S06837; S06837.  
 DR PDR; IGEC; 07-DEC-95.  
 DP MEROPS; C01.004.  
 DR InterPro; IPR000668; Peptidase C1.  
 DR InterPro; IPR000169; SHprot\_acsite.  
 DR Pfam; PF00112; Peptidase C1; 1.  
 DR PRINTS; PR00705; PAPAIN.  
 DR ProDom; PD000158; Peptidase C1; 1.  
 DR PROSITE; PS00139; THIOL PROTEASE CYS; 1.  
 DR PROSITE; PS00639; THIOL PROTEASE HIS; 1.  
 DR PROSITE; PS00640; THIOL PROTEASE ASN; 1.  
 KW Hydrolase, Thiol protease, Cysteine, Signal, 3D-structure.  
 FT SIGNAL 1 18 POTENTIAL.  
 FT PROPEP 19 132 ACTIVATION PEPTIDE.  
 FT CHAIN 133 348 PAPAYA PROTEINASE IV.  
 FT ACT\_SITE 157 157 BY SIMILARITY.  
 FT ACT\_SITE 291 291 BY SIMILARITY.  
 FT ACT\_SITE 311 311 BY SIMILARITY.  
 FT DISULFID 154 195  
 FT DISULFID 188 227  
 FT DISULFID 285 336  
 FT CONFLICT 190 190  
 SQ SEQUENCE 344 AA; 30024 MW; 4085EEDE37F69ASE CRC64;  
 K -> L (IN REF. 2).  
 Query Match 21.0%; Score 355.5; DB 1; Length 348;  
 Best Local Similarity 30.4%; Pred. No. 2.5e-21;  
 Matches 89; Conservative 58; Mismatches 115; Indels 31; Gaps 12;  
 QY 23 IETLETFYFANKEVATFECEAAAPKPLESVYVYV-----NQG AINHLSDLSLDER 75  
 DB 45 IGFENSWVFENFNN-NVDF-LVFEFPEFENLEFIDENMINYMWLSNEFSLSNDEF 104  
 DY 76 ENEDLMGAFAPFHEFETLFD-----INAFNASEINENNAVALICLL-METVYTIEM-336-350 142

DB 106 KFYVWGLPE-DVTNQPPYFFENFNY-----VNEPFEVWEAFVATVAPVCEVESC 157  
 QY 133 WAFGGVAALISAYLAIRNGLLLAEDELVLCAAT-HSHHGLTIRPMIAYLHNNVWVASY 191  
 FE 134 WAFSTVATVNTNIP-FTHQVETSEAFNATVTPKLVSSMSVQCT-ITVAAGSHLPAF 217  
 QY 132 YEVVAREQSGRR-----ENAKRISLSNIQITFEENVNRIEALATHSALAVITITKID 246  
 LE 218 YETIAT-ETTPAKVAGVTPVTHVAT-FAV-NVEVLLNDAIA-KLVVYVVEKAR 321  
 QY 247 AHHHL-ETITLIDENGL-ENTHRAVIVLVLGAKASHVWVVERKWLNNWJGNS 299  
 FE 276 FENYVQ NIFERSSNTNFI HAVIAYVWVTPKLVVILFVFLFWNOMGNS 322

Search completed: Mar 10, 2003, 09:52:24  
 Job time : 41.6689 secs





QY 1 MMTVITATASLALSAVAYAPPSSIFTEETEEYFAENKSYATFEDEEAAAFNLESVYVYVSN 60  
 DB 1 MMTVITATASLALSAVAYAPPSSIFTEETEEYFAENKSYATFEDEEAAAFNLESVYVYVSN 60  
 QY 61 GGAINHLSLUSLDEPFRFELMSABEFHLSKTOEDLNATNACINENAPAEIDLPQRTV 120  
 DB 61 GGAINHLSLUSLDEPFRFELMSABEFHLSKTOEDLNATNACINENAPAEIDLPQRTV 120  
 QY 121 TPIMWQSGSGSWAFSGVAATESAYLAHNPQSLDLAEQELVDCASQCHGCHOTPPGIEY 180  
 DB 121 TPIMWQSGSGSWAFSGVAATESAYLAHNPQSLDLAEQELVDCASQCHGCHOTPPGIEY 180  
 QY 181 ICHNGVQESYVYVAFEGSCPPNACPPGISNYQIYPPNNWIPREALACTHSAIAVII 240  
 DB 181 ICHNGVQESYVYVAFEGSCPPNACPPGISNYQIYPPNNWIPREALACTHSAIAVII 240  
 QY 241 GIKELDAFFSHVDCETIIFORNGYQENYHATIVGVSNACQTVWIVNMTWKTWYNGY 300  
 DB 241 GIKELDAFFSHVDCETIIFORNGYQENYHATIVGVSNACQTVWIVNMTWKTWYNGY 300  
 QY 301 YFAANIDLMIEEYVYVIL 320  
 DB 301 YFAANIDLMIEEYVYVIL 320

## RESULT 2

US-08-462-831-10  
 : Sequence 10, Application US/08462831  
 : Patent No. 5522142  
 : GENERAL INFORMATION:  
 : APPLICANT:  
 : TITLE OF INVENTION: 7 CELL EPITOPES OF THE MAMM ALLELGENS FROM  
 : TITLE OF INVENTION: DERMATOPHAGOCYTES  
 : NUMBER OF SEQUENCES: 13  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: LAHIVE & COCKFIELD  
 : STREET: 60 STATE STREET, SUITE 510  
 : CITY: BOSTON  
 : STATE: MA  
 : COUNTRY: USA  
 : ZIP: 02109  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: ASCII TEXT  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US 08/462,831  
 : FILING DATE:  
 : CLASSIFICATION: 424  
 : PPI/P APPLICATION DATA:  
 : APPLICATION NUMBER: US 07/945,288  
 : FILING DATE: 10 SEPTEMBER 1992  
 : APPLICATION NUMBER: US 580,655  
 : FILING DATE: 11 SEPTEMBER 1990  
 : APPLICATION NUMBER: US 458,642  
 : FILING DATE: 13 FEBRUARY 1990  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: MANDACOURAS, AMY E.  
 : REGISTRATION NUMBER: 36,207  
 : REFERENCE/AGENT NUMBER: IP-1000 (IMI-024)  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: (617) 227-7400  
 : TELEFAX: (617) 227-5941  
 : INFORMATION FOR SEQ ID NO: 10:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 320 amino acids  
 : TYPE: amino acid  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: protein  
 : US-08-462-831-10

Query Match

us 08 462 831 10

Post-Translational Similarity 99.1%; P-rod No. 6-50-169;  
 Matches 317; Conservative 17; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 MMTVITATASLALSAVAYAPPSSIFTEETEEYFAENKSYATFEDEEAAAFNLESVYVYVSN 60  
 DB 1 MMTVITATASLALSAVAYAPPSSIFTEETEEYFAENKSYATFEDEEAAAFNLESVYVYVSN 60  
 QY 61 GGAINHLSLUSLDEPFRFELMSABEFHLSKTOEDLNATNACINENAPAEIDLPQRTV 120  
 DB 61 GGAINHLSLUSLDEPFRFELMSABEFHLSKTOEDLNATNACINENAPAEIDLPQRTV 120  
 QY 121 TPIMWQSGSGSWAFSGVAATESAYLAHNPQSLDLAEQELVDCASQCHGCHOTPPGIEY 180  
 DB 121 TPIMWQSGSGSWAFSGVAATESAYLAHNPQSLDLAEQELVDCASQCHGCHOTPPGIEY 180  
 QY 181 ICHNGVQESYVYVAFEGSCPPNACPPGISNYQIYPPNNWIPREALACTHSAIAVII 240  
 DB 181 ICHNGVQESYVYVAFEGSCPPNACPPGISNYQIYPPNNWIPREALACTHSAIAVII 240  
 QY 241 GIKELDAFFSHVDCETIIFORNGYQENYHATIVGVSNACQTVWIVNMTWKTWYNGY 300  
 DB 241 GIKELDAFFSHVDCETIIFORNGYQENYHATIVGVSNACQTVWIVNMTWKTWYNGY 300  
 QY 301 YFAANIDLMIEEYVYVIL 320  
 DB 301 YFAANIDLMIEEYVYVIL 320

## RESULT 3

US-08-461-809-10  
 : Sequence 10, Application US/08461809  
 : Patent No. 5770002  
 : GENERAL INFORMATION:  
 : APPLICANT:  
 : TITLE OF INVENTION: 7 CELL EPITOPES OF THE MAMM ALLELGENS FROM  
 : TITLE OF INVENTION: DERMATOPHAGOCYTES  
 : NUMBER OF SEQUENCES: 13  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: LAHIVE & COCKFIELD  
 : STREET: 60 STATE STREET, SUITE 510  
 : CITY: BOSTON  
 : STATE: MA  
 : COUNTRY: USA  
 : ZIP: 02109  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: ASCII TEXT  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US 08/461,809  
 : FILING DATE:  
 : CLASSIFICATION: 424  
 : PPI/P APPLICATION DATA:  
 : APPLICATION NUMBER: US 07/945,288  
 : FILING DATE: 10 SEPTEMBER 1992  
 : APPLICATION NUMBER: US 580,655  
 : FILING DATE: 11 SEPTEMBER 1990  
 : APPLICATION NUMBER: US 458,642  
 : FILING DATE: 13 FEBRUARY 1990  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: MANDACOURAS, AMY E.  
 : REGISTRATION NUMBER: 36,207  
 : REFERENCE/AGENT NUMBER: IP-1000 (IMI-024)  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: (617) 227-7400  
 : TELEFAX: (617) 227-5941  
 : INFORMATION FOR SEQ ID NO: 10:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 320 amino acids  
 : TYPE: amino acid  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: protein

US 09 461 809-10

Query Match: 99.23; Score 1676; E.E. 1; Length 320;  
 Best Local Similarity 99.18; Pct. No. 5.5e 169;  
 Matches 317; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKVLAIAALSAVYAPFESKTEEFVFAFNFVATFECEFAAFNFLEFVYVQCN 60  
 DB 1 MKVLAIAALSAVYAPFESKTEEFVFAFNFVATFECEFAAFNFLEFVYVQCN 60  
 QY 61 GGAINHLSLSLDEPKPFELMSAEAFELHTFTDLNAETNACISINAPAEIDPOMETV 120  
 DB 61 GGAINHLSLSLDEPKPFELMSAEAFELHTFTDLNAETNACISINAPAEIDPOMETV 120  
 QY 121 TPFMQGGGSCWAFESVVAATESAYLAENQSLDLAEELVDCASQHGSGHIIPEGLEY 180  
 DB 121 TPFMQGGGSCWAFESVVAATESAYLAENQSLDLAEELVDCASQHGSGHIIPEGLEY 180  
 QY 181 IQHNGVVQESYVYVAPEQSCPPNAQPSISNYQIYPPNVNFKKALAQTHSAIAVII 240  
 DB 181 IQHNGVVQESYVYVAPEQSCPPNAQPSISNYQIYPPNVNFKKALAQTHSAIAVII 240  
 QY 241 GIKELAFPHVQDFTIIEINFTINHTANVYVNSNACINVTWVFNKWTNWNENYV 300  
 DB 241 GIKELAFPHVQDFTIIEINFTINHTANVYVNSNACINVTWVFNKWTNWNENYV 300  
 QY 301 YFAANIDLMIEEYPYVWIL 320  
 DB 301 YFAANIDLMIEEYPYVWIL 320

## RESULT 4

US 09-461 441-10  
 : Sequence 10, Application US/09461441  
 : Patent No. 5773062  
 : GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS FROM

DERMATOPHAGOIDES

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSES: LARIVE & COMPANY

STREET: 60 STATE STREET, SUITE 510

CITY: BOSTON

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII TEXT

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/461,441

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/945,288

FILING DATE: 10 SEPTEMBER 1992

APPLICATION NUMBER: US 580,655

FILING DATE: 11 SEPTEMBER 1990

APPLICATION NUMBER: US 459,642

FILING DATE: 13 FEBRUARY 1990

ATTORNEY/AGENT INFORMATION:

NAME: MANDRAGOURAS, AMY E.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: IPC-0100C (IMI-024)

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO. 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 320 amino acids

TOPOLOGY: linear

TYPE: amino acid  
 TOPOLOGY: linear  
 M-TERM TYPE: Protein  
 US 09-461-441-10

Query Match: 99.23; Score 1676; E.E. 1; Length 320;

Best Local Similarity 99.18; Pct. No. 5.5e 169;

Matches 317; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKVLAIAALSAVYAPFESKTEEFVFAFNFVATFECEFAAFNFLEFVYVQCN 60  
 DB 1 MKVLAIAALSAVYAPFESKTEEFVFAFNFVATFECEFAAFNFLEFVYVQCN 60  
 QY 61 GGAINHLSLSLDEPKPFELMSAEAFELHTFTDLNAETNACISINAPAEIDPOMETV 120  
 DB 61 GGAINHLSLSLDEPKPFELMSAEAFELHTFTDLNAETNACISINAPAEIDPOMETV 120  
 QY 121 TPFMQGGGSCWAFESVVAATESAYLAENQSLDLAEELVDCASQHGSGHIIPEGLEY 180  
 DB 121 TPFMQGGGSCWAFESVVAATESAYLAENQSLDLAEELVDCASQHGSGHIIPEGLEY 180  
 QY 181 IQHNGVVQESYVYVAPEQSCPPNAQPSISNYQIYPPNVNFKKALAQTHSAIAVII 240  
 DB 181 IQHNGVVQESYVYVAPEQSCPPNAQPSISNYQIYPPNVNFKKALAQTHSAIAVII 240  
 QY 241 GIKELAFPHVQDFTIIEINFTINHTANVYVNSNACINVTWVFNKWTNWNENYV 300  
 DB 241 GIKELAFPHVQDFTIIEINFTINHTANVYVNSNACINVTWVFNKWTNWNENYV 300  
 QY 301 YFAANIDLMIEEYPYVWIL 320  
 DB 301 YFAANIDLMIEEYPYVWIL 320

## RESULT 5

PCT-US93-08518-10

: Sequence 10, Application PCT/US9308518

: GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS FROM

DERMATOPHAGOIDES

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSES: LARIVE & COMPANY

STREET: 60 STATE STREET, SUITE 510

CITY: BOSTON

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII TEXT

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/08518

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/945,288

FILING DATE: 10 SEPTEMBER 1992

APPLICATION NUMBER: US 580,655

FILING DATE: 11 SEPTEMBER 1990

APPLICATION NUMBER: US 459,642

FILING DATE: 13 FEBRUARY 1990

ATTORNEY/AGENT INFORMATION:

NAME: MANDRAGOURAS, AMY E.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: IPC-0100C (IMI-024)

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO. 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 320 amino acids

TOPOLOGY: linear

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LENGTH: 322 amino acids

1617  
1618



INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 321 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US 08 462-831-6

Query Match 84.4% Score 1425.5; DB 1; Length 321;  
 Best Local Similarity 82.9%, Pred. No. 26 142;  
 Matches 266; Conservative 25; Mismatches 29; Indels 1; Gaps 1;

QY 1 MFTVLATASLLASAVYATGSSSTTETFFPAFNSSTAFEELEAAAFNPLFADYVAVN 60  
 DB 1 MFTVLATASLLVSTVYAPASITFTFFPPAFNPTATVEEVEVAPNFELEFYVEAN 60  
 QY 61 GSAINHLSDLSLGEFNFPLMSAEAFERKTFPLAAETNATNSIN-NADA-IRHQMHT 119  
 DB 61 KCAINHLSDYISITFFNPYLSAEAEQELKPELNALISAERINLVHVESLEMSERT 120  
 QY 120 VTFPMQGGGSGTWAFSGVAATESAYLAYENQSLDLAEQLVQASQGGSGSTIFRGI 179  
 DB 121 VTFPMQGGGSGTWAFSGVAATESAYLAYENQSLDLAEQLVQASQGGSGSTIFRGI 180  
 QY 180 YIQNGVVEESYFYVAKEQKRENSQHYGISNAGIYPPDVFQIPEALITHTAIAVI 240  
 DB 181 YIQNGVVEESYFYVAKEQKRENSQHYGISNAGIYPPDVFQIPEALITHTAIAVI 240  
 QY 240 TGIKLEAFERHDEGRTITTFPMQGVYHVNINYN-NAGVYVIVNSWENKINW 299  
 DB 241 TGIKLRAPQHYGRTITTFPMQGVYHVNINYN-NAGVYVIVNSWENKINW 300  
 QY 300 GYPAANIDLMIEEYPYVIL 320  
 DB 301 GYFGAGNNLMIEQYPYVIM 321

RESULT 8  
 US 08 461-809-6  
 Sequence 6, Application US/08461809  
 Patent No. 5770202

GENERAL INFORMATION:  
 APPLICANT:  
 TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLELGENS FROM  
 TITLE OF INVENTION: DERMATOPHAGOCYTES  
 NUMBER OF SEQUENCES: 13  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: LAHIVE & COCKFIELD  
 STREET: 60 STATE STREET, SUITE 510  
 CITY: BOSTON  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: ASCII TEXT  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/461 809  
 FILING DATE:  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/945,288  
 FILING DATE: 10 SEPTEMBER 1992  
 APPLICATION NUMBER: US 580,655  
 FILING DATE: 11 SEPTEMBER 1990  
 APPLICATION NUMBER: US 458,642  
 FILING DATE: 13 FEBRUARY 1990  
 NAME: MANDRAGOURAS, AMY E.  
 REGISTRATION NUMBER: 36,207  
 REFERENCE/AGENT NUMBER: IPC CLASS (X) 824)

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 321 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-461-809-6

Query Match 84.4% Score 1425.5; DB 1; Length 321;

Best Local Similarity 82.9%, Pred. No. 26 142;

Matches 266; Conservative 25; Mismatches 29; Indels 1; Gaps 1;

QY 1 MFTVLATASLLASAVYATGSSSTTETFFPAFNSSTAFEELEAAAFNPLFADYVAVN 60  
 DB 1 MFTVLATASLLVSTVYAPASITFTFFPPAFNPTATVEEVEVAPNFELEFYVEAN 60  
 QY 61 GSAINHLSDLSLGEFNFPLMSAEAFERKTFPLAAETNATNSIN-NADA-IRHQMHT 119  
 DB 61 KCAINHLSDYISITFFNPYLSAEAEQELKPELNALISAERINLVHVESLEMSERT 120  
 QY 120 VTFPMQGGGSGTWAFSGVAATESAYLAYENQSLDLAEQLVQASQGGSGSTIFRGI 179  
 DB 121 VTFPMQGGGSGTWAFSGVAATESAYLAYENQSLDLAEQLVQASQGGSGSTIFRGI 180  
 QY 180 YIQNGVVEESYFYVAKEQKRENSQHYGISNAGIYPPDVFQIPEALITHTAIAVI 240  
 DB 181 YIQNGVVEESYFYVAKEQKRENSQHYGISNAGIYPPDVFQIPEALITHTAIAVI 240  
 QY 240 TGIKLEAFERHDEGRTITTFPMQGVYHVNINYN-NAGVYVIVNSWENKINW 299  
 DB 241 TGIKLRAPQHYGRTITTFPMQGVYHVNINYN-NAGVYVIVNSWENKINW 300  
 QY 300 GYPAANIDLMIEEYPYVIL 320  
 DB 301 GYFGAGNNLMIEQYPYVIM 321

RESULT 9

US-08-461-441-6

Sequence 6, Application US/08461441

Patent No. 5773002

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLELGENS FROM

TITLE OF INVENTION: DERMATOPHAGOCYTES

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESS: LAHIVE & COCKFIELD

STREET: 60 STATE STREET, SUITE 510

CITY: BOSTON

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII TEXT

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/461 441

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/945,288

FILING DATE: 10 SEPTEMBER 1992

APPLICATION NUMBER: US 580,655

FILING DATE: 11 SEPTEMBER 1990

APPLICATION NUMBER: US 458,642

FILING DATE: 13 FEBRUARY 1990

NAME: MANDRAGOURAS, AMY E.

REGISTRATION NUMBER: 36,207

REFERENCE/AGENT INFORMATION:



```

1 MEDIUM TYPE: Floppy disk
2 COMPUTER: IBM PC compatible
3 OPERATING SYSTEM: PC-MS/MS-DOS
4 SOFTWARE: ASCII TEXT
5 CURRENT APPLICATION DATA:
6 APPLICATION NUMBER: 11-004/478,572
7 FILING DATE: 07-June-1995
8 CLASSIFICATION:
9 PRIOR APPLICATION DATA:
10 APPLICATION NUMBER: 08/445,307
11 FILING DATE:
12 ATTORNEY/AGENT INFORMATION:
13 NAME: CRAIG, ANNE I.
14 REGISTRATION NUMBER: 32,978
15 REFERENCE/DOCKET NUMBER: 017,615
16 TELECOMMUNICATION INFORMATION:
17 TELEPHONE: (617) 466-6000
18 TELEFAX: (617) 466-6040
19 INFORMATION FOR SEQ ID NO: 6:
20 SEQUENCE CHARACTERISTICS:
21 LENGTH: 121 amino acids
22 TYPE: amino acid
23 TOPOLOGY: linear
24 MOLECULE TYPE: protein
25
26 US 08,478,572-6

```

|                       |              |                 |               |            |
|-----------------------|--------------|-----------------|---------------|------------|
| Query Match           | 94.4%        | Score 1425.5    | EB 2          | Length 321 |
| Best local Similarity | 92.9%        | Pred. No. 2e142 |               |            |
| Matches 266           | Conservative | 25              | Mismatches 23 | Indels 1   |

[illegible]

## RESULT 12

US 98-484-296 6  
Sequence 6, Applicant No. 98/09494296  
Patent No. 6268491

GENERAL INFORMATION:

APPLICANT: Garman, Richard  
APPLICANT: Greenstein, Julia  
APPLICANT: Kuo, Mei-Chang  
APPLICANT: Rogers, Bruce  
APPLICANT: Rozen, Henry  
APPLICANT: Chen, Xian  
APPLICANT: Evans, Zeev  
APPLICANT: Shaked, Zeev

1 TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLELGENS  
2  
3 TITLE OF INVENTION: FROM DERMATOPHAGOIDES (HOUSE DUST MITE)  
4  
5 NUMBER OF SEQUENCES: 207  
6  
7 CORRESPONDENCE ADDRESS:  
8 ADDRESSEE: IMMUNOLOGIC PHARMACEUTICAL CORPORATION

STREET: 610 LINCOLN STREET  
CITY: WALTHAM  
STATE: MA  
COUNTRY: USA  
ZIP: 02154  
COMPUTER RECAUSE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII TEXT  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: 09/69/484,296  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/445,187  
FILING DATE: 07 June 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: CRAIG, ANNE I.  
REGISTRATION NUMBER: 32,976  
REFERENCE/DOCKET NUMBER: 017,615  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 466-6000  
TELEFAX: (617) 466-6040  
INFORMATION FOR SEQ ID NO. 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 321 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

Query Match: 84.4%, Score 1422.5, DB 4; Length 321;

Best Local Similarity 92.9%, Pred. No. 2e-142;

Matches 266, Conservative 25, Mismatches 29, Indels 1, Gaps 1;

[illegible]

300 GYFAANTDI.MMTFFYBPVVTL 320

[illegible]

DB 301 GYFQAGNNLMMIEQYPYVIM 321

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RESULT 13
PCT-US93-04518-6
; Sequence 6, Application PC/TUS9309518
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: CELL ELUTION FROM
; TITLE OF INVENTION: WATER ALKALINE FROM
; TITLE OF INVENTION: DERMATOPHAGOIDES

```

ADDRESS: LAHIVE & COCKFIELD  
STREET: 60 STATE STREET, SUITE 510  
CITY: BOSTON







GenCore version 5.1.4.P5.4578  
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OM protein: protein search, using SW Model

Run on: March 12, 2003, 08:41:15 : Search time 22.194 seconds  
(without alignments)  
605.141 Million cell updates/sec

Title: UC-05-877-160-3

Perfect score: 773  
Sequence: 1 MMWKLICLLLVAAVAPDGV

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post processing: Minimum Match 14  
Maximum Match 1000  
Listing first 45 summaries

Databases :

1: PIR 73.4  
2: PIR1.4  
3: PIR3.4  
4: PIR4.4

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID    | Description        |
|------------|-------|-------------|--------|----------|--------------------|
| 1          | 773   | 100.0       | 146    | 2 A60381 | allergen Der p II  |
| 2          | 653   | 84.0        | 138    | 2 E61241 | allergen Der p II  |
| 3          | 653   | 84.5        | 138    | 2 A61241 | allergen Der p II  |
| 4          | 630   | 81.5        | 129    | 2 A61344 | allergen Der p II  |
| 5          | 624   | 80.7        | 129    | 2 A61501 | allergen Der p II  |
| 6          | 278.5 | 16.0        | 141    | 2 S65504 | allergen Der p I   |
| 7          | 274.5 | 15.5        | 141    | 2 S65499 | allergen Der p I   |
| 8          | 123   | 15.9        | 151    | 2 I36896 | epididymal secret  |
| 9          | 123   | 15.9        | 151    | 2 I53929 | epididymal secret  |
| 10         | 115.5 | 14.9        | 146    | 2 T33404 | hypothetical prote |
| 11         | 105   | 13.6        | 149    | 2 I69229 | epididymal secret  |
| 12         | 89    | 11.5        | 151    | 2 A64503 | conserved hypothet |
| 13         | 86.5  | 11.2        | 577    | 2 B37057 | integrin beta-5 ch |
| 14         | 79.5  | 10.3        | 788    | 2 A37057 | integrin beta-6 ch |
| 15         | 79.5  | 10.3        | 788    | 2 T21140 | hypothetical prote |
| 16         | 78    | 10.1        | 249    | 2 S75749 | hypothetical prote |
| 17         | 76.5  | 9.5         | 494    | 2 A61154 | conserved membrane |
| 18         | 76    | 9.8         | 175    | 1 DZ211X | gene 1 protein - M |
| 19         | 75.5  | 9.8         | 410    | 2 C96803 | hypothetical prote |
| 20         | 75.5  | 9.8         | 486    | 2 AE1514 | conserved membrane |
| 21         | 75.5  | 9.8         | 6805   | 2 S29901 | titin - rabbit (fr |
| 22         | 75    | 9.7         | 1307   | 2 T34702 | hypothetical prote |
| 23         | 74.5  | 9.6         | 324    | 2 T10394 | cathepsin - Orgyia |
| 24         | 74.5  | 9.6         | 362    | 2 A60789 | protein G3496.5 li |
| 25         | 74.5  | 9.6         | 2555   | 2 A40043 | notch protein homo |
| 26         | 74    | 9.6         | 381    | 2 S39196 | beta-lactamase (EC |
| 27         | 73.5  | 9.4         | 2104   | 1 I54421 | aggrexin precursor |
| 28         | 73    | 9.4         | 407    | 2 C69023 | conserved hypothet |
| 29         | 73    | 9.4         | 1188   | 2 T13933 | pol polyprotein -  |

#### ALIGNMENTS

##### RESULT 1

A60381  
allergen Der p II precursor - house dust mite (dermatophagoides pteronyssinus)  
C:Species: Dermatophagoides pteronyssinus  
C:Date: 11 Mar 1994 #Sequence: 1181193 #Accession: A60381  
C:Accession: A60381  
P:Chen, Y. Y., Doyle, C. P., Simpson, P. J., Turner, P. J., Stewart, G. A., Thomas, W. R.  
Int. Arch. Allergy Appl. Immunol. 91, 118-123, 1990  
A:Title: Isolation of cDNA coding for the major whe allergen Der p II by IgE plaque imm  
A:Reference number: A60381; MIM: 60254201; PMID: 2341191  
A:Accession: A60381  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-146 <CHUS>  
C:Superfamily: allergen Der p II  
F:1-17/Domain: signal sequence #status predicted <SIG>  
F:19-146/Product: allergen Der p II #status predicted <MAT>

Query Match 100.0%, Score 773, DB 2, Length 146;  
Best Local Similarity 100.0%, Pred No 14-69;  
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMWKLICLLLVAAVAPDGVVDCANHEIKVLVPGCHGSEPCIIHPGKFGLEAVPEA 60  
LP 1 MMWKLICLLLVAAVAPDGVVDCANHEIKVLVPGCHGSEPCIIHPGKFGLEAVPEA 60  
QY 61 NNTPTAPTEIEKASTGSEFVTVGEGIFVAKTVMWTFIVVGVTVVTVWSPPTAPSEEN 120  
LP 61 NNTPTAPTEIEKASTGSEFVTVGEGIFVAKTVMWTFIVVGVTVVTVWSPPTAPSEEN 120  
QY 101 VVVTVVWMTGVLAATATATATATATATATATATATATATATATATATATATATAT 146  
LP 101 VVVTVVWMTGVLAATATATATATATATATATATATATATATATATATATATATAT 146

##### RESULT 2

B61241  
allergen Der p II precursor - house dust mite (dermatophagoides farinae)  
C:Species: Dermatophagoides farinae  
C:Date: 11 May 1994 #Sequence: 1181193 #Accession: B61241  
C:Accession: B61241; J00395  
P:Tsukui, T., Okumura, Y., Ando, T., Yamakawa, H., Sako, M., Haida, M., Dohi, M., Okudaira  
Int. Arch. Allergy Appl. Immunol. 94, 354-356, 1991  
A:Title: Synthesis of biologically active recombinant Der p II.  
A:Reference number: A61241; MIM: 6040791; PMID: 1937898  
A:Accession: B61241  
A:Molecule type: mRNA  
A:Residues: 1-139 <YUUS>  
C:Superfamily: allergen Der p II  
F:1-9/Domain: signal sequence #status predicted <SIG>  
F:10-139/Product: allergen Der p II #status predicted <MAT>

Notch 1 protein -  
fimbrial adhesin f  
hypothetical prote  
hypothetical prote  
structural polypro  
heat shock protein  
hypothetical prote  
beta lactamase (EC  
flav mon oxidase  
irin, cardiac mus  
glycine membrane  
beta lactamase (EC  
6-phosphofructo-2-  
hypothetical prote  
adenosylmethioni

Query Match: 84.28, Score 652, DB 2, Length 135;  
 Best Local Similarity: 87.78, Pred. No. 4.3e-58;  
 Matches: 121, Conservative: 11, Mismatches: 5, Indels: 0, Gaps: 0

QY 2 ALLVAATVAVDQVYVFAHETITVVLVFGGSGSPPTTHSPTTLEAVPEAKHNTTAY 68  
 DE 1 ALLVAATVAVDQVYVFAHETITVVLVFGGSGSPPTTHSPTTLEAVPEAKHNTTAY 68

CY 2 LEIIVAGISLELVFVSHCHVMTFLVPSGQVLYFTWVVTAFPSSENVVTVFM 128  
 DB 61 LEIIVAGISLELVFVSHCHVMTFLVPSGQVLYFTWVVTAFPSSENVVTVFM 128

QY 129 GDOGVLAIAIATHAKIRD 146  
 DB 121 GDOGVLAIAIATHAKIRD 139

RESULT 3  
 A61241  
 allergen Der f II precursor house dust mite (Dermatophagoides farinae) (fragment)  
 C:Species: Dermatophagoides farinae  
 C>Date: 12 May 1994 #sequence\_revision: 27 Jan 1994 #text\_change: 11-Sep-1994  
 C:Accession: A61241, F56417  
 R:Yukita, T.; Okumura, Y.; Ando, T.; Yokokawa, H.; Suko, M.; Haida, M.; Dobai, M.; Okudaira, H.; Arch. Allergy Appl. Immunol. 94, 254-256, 1991  
 A:Title: Synthesis of biologically active recombinant Der f II.  
 A:Reference number: A61241; MUID:92040281; PMID:1937998  
 A:Accession: A61241  
 A:Molecule type: mRNA  
 A:Residues: 1-129 <YU>  
 A:Note: Part of this sequence, including the main end of the mature protein, was confirmed by the allergen Der f II  
 E1:9/Domain: signal sequence (fragment) #status: predicted <SIG>  
 E1:135/Domain: allergen Der f II #status: experimental <MAT>

Query Match: 94.58, Score 653, DB 2, Length 139;  
 Best Local Similarity: 87.08, Pred. No. 8.6e-58;  
 Matches: 126, Conservative: 10, Mismatches: 5, Indels: 0, Gaps: 0

QY 2 ALLVAATVAVDQVYVFAHETITVVLVFGGSGSPPTTHSPTTLEAVPEAKHNTTAY 68  
 DE 1 ALLVAATVAVDQVYVFAHETITVVLVFGGSGSPPTTHSPTTLEAVPEAKHNTTAY 68

CY 2 LEIIVAGISLELVFVSHCHVMTFLVPSGQVLYFTWVVTAFPSSENVVTVFM 128  
 DB 61 LEIIVAGISLELVFVSHCHVMTFLVPSGQVLYFTWVVTAFPSSENVVTVFM 128

QY 129 GDOGVLAIAIATHAKIRD 146  
 DB 121 GDOGVLAIAIATHAKIRD 139

RESULT 4  
 J00394  
 allergen Der f II (p12) house-dust mite (Dermatophagoides farinae)  
 C:Species: Dermatophagoides farinae  
 C>Date: 30 Sep 1991 #sequence\_revision: 30-Sep-1991 #text\_change: 17-Mar-1999  
 C:Accession: J00394  
 R:Yukita, T.; Okumura, Y.; Ando, T.; Yokokawa, H.; Suko, M.; Haida, M.; Okudaira, H.; Agric. Biol. Chem. 55, 2223-2229, 1991  
 A:Title: Cloning and expression of cDNA coding for the major house dust mite allergen Der f II.  
 A:Reference number: F56417, MUID:92040281, PMID:1369682  
 A:Accession: J00394  
 A:Molecule type: mRNA  
 A:Residues: 1-129 <YU>  
 A:Superfamily: allergen Der p II

Query Match: 81.58, Score 630, DB 2, Length 129;  
 Best Local Similarity: 88.48, Pred. No. 1.6e-55;  
 Matches: 114, Conservative: 11, Mismatches: 4, Indels: 0, Gaps: 0

QY 19 GDOGVLAIAIATHAKIRD 146  
 DB 121 GDOGVLAIAIATHAKIRD 139

QY 1 GDOGVLAIAIATHAKIRD 146  
 DB 121 GDOGVLAIAIATHAKIRD 139

QY 129 GDOGVLAIAIATHAKIRD 146  
 DB 121 GDOGVLAIAIATHAKIRD 139

RESULT 5  
 A61501  
 allergen Der f II - house-dust mite (Dermatophagoides farinae) (fragment)  
 C:Species: Dermatophagoides farinae  
 C>Date: 07-Oct-1994 #sequence\_revision: 07-Oct-1994 #text\_change: 13-Sep-1998  
 C:Accession: A61501  
 R:Trudinger, M.; Chua, K.Y.; Thomas, W.R.  
 Clin. Exp. Allergy 21, 33-37, 1991  
 A:Title: cDNA encoding the major mite allergen Der f II.  
 A:Reference number: A61501; MUID:91215495; PMID:2021874  
 A:Accession: A61501  
 A:Molecule type: mRNA  
 A:Status: preliminary, not compared with conceptual translation  
 A:Residues: 1-129 <TPU>  
 C:Superfamily: allergen Der p II

Query Match: 80.78, Score 624, DB 2, Length 129;  
 Best Local Similarity: 87.68, Pred. No. 6.2e-55;  
 Matches: 113, Conservative: 11, Mismatches: 5, Indels: 0, Gaps: 0

QY 19 GDOGVLAIAIATHAKIRD 146  
 DE 1 ALLVAATVAVDQVYVFAHETITVVLVFGGSGSPPTTHSPTTLEAVPEAKHNTTAY 68

CY 2 LEIIVAGISLELVFVSHCHVMTFLVPSGQVLYFTWVVTAFPSSENVVTVFM 128  
 DB 61 LEIIVAGISLELVFVSHCHVMTFLVPSGQVLYFTWVVTAFPSSENVVTVFM 128

QY 79 LEIVVPGTIDNACHVMTFLVPSGQVLYFTWVVTAFPSSENVVTVFM 137  
 DE 1 LEIVVPGTIDNACHVMTFLVPSGQVLYFTWVVTAFPSSENVVTVFM 137

QY 139 IATHAKIRD 146  
 DE 121 IATHAKIRD 139

RESULT 6  
 S64560  
 allergen Lep d I 01 precursor (clone d 1 0102) - Lepidoglyphus destructor  
 C:Species: Lepidoglyphus destructor  
 C>Date: 19-Mar-1997 #sequence\_revision: 19-Mar-1997 #text\_change: 20-Sep-1999  
 C:Accession: S64560, S48727, S66034  
 R:Schmidt, M.; Olsson, S.; van der Ploeg, I.; van Hage-Hamsten, M.; FEBS Lett. 370, 11-14, 1995  
 A:Title: cDNA analysis of the mite allergen Lep d I identifies two different isoallergens  
 A:Reference number: S64560, S48727, S66034  
 A:Accession: S64560  
 A:Molecule type: mRNA  
 A:Residues: 1-141 <SCH>  
 A:Cross-references: EMP1:Y99014; NID:900451; PIR:AA1416 1; PIR:Q99022  
 R:Varela, J.; Ventas, F.; Garcia, C.; Barbas, J.; Gimenez Gallego, C.; Polo, F.; Pur. J. Biochem. 225, 93-98, 1994  
 A:Title: Primary structure of Lep d I, the main lepidoglyphus destructor allergen.  
 A:Reference number: S64560, MUID:9010146, PMID:905475  
 A:Accession: S48727  
 A:Molecule type: mRNA  
 A:Residues: 44-141 <VAV>  
 A:Cross-references: EMBL:X91393, NID:958743, PIR:Q99016 1; PIR:Q990450  
 A:Accession: S66034  
 A:Molecule type: protein  
 A:Residues: 17-140 <VAR>  
 A:Note: 83 Asp, 53 Asn, 66 His, 104-Lys, 104-Asn, 104-Val were also found  
 C:Superfamily: allergen Der p II  
 E1:135/Domain: signal sequence Heratus predicted <SIG>  
 E1:17-140/Domain: allergen Lep d I 01 #status: experimental <MAT>



|                          |       |                |           |             |
|--------------------------|-------|----------------|-----------|-------------|
| Query March              | 36.0% | Score 278.5;   | DB 2;     | Length 141; |
| Best Local Similarity    | 37.2% | RefSeq 2.892%  |           |             |
| Matches 53; Conservative | 33;   | Mismatches 54; | Indels 3; | Gaps 1;     |







# SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: \_\_\_\_\_  
 Art Unit: \_\_\_\_\_  
 Phone Number (30) \_\_\_\_\_  
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 Date: \_\_\_\_\_  
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**If more than one search is submitted, please prioritize searches in order of need.**

\*\*\*\*\*  
 Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, key words, synonyms, and registry numbers, and combine with the concept or unity of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc. if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: \_\_\_\_\_  
 Inventors (please provide full names): \_\_\_\_\_  
 Earliest Priority Filing Date: \_\_\_\_\_

*\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Jan Delaval  
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| Lexis Nexis                 | _____ |
| Sequence Systems            | _____ |
| WWW Internet                | _____ |
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| Litigation                  | _____ |
| Structure (#)               | _____ |
| Structure (M)               | _____ |
| Other                       | _____ |

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Mary Hale, Supervisor, 308-4258  
CM-1 Room 1101

### Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: (Example: 1610)

➤ Relevant prior art found, search results used as follows:

☐ 102 rejection

☐ 103 rejection

☐ Cited as being of interest.

☐ Helped examiner better understand the invention.

☐ Helped examiner better understand the state of the art in their technology.

*Types of relevant prior art found:*

☐ Foreign Patent(s)

☐ Non-Patent Literature

(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art not found:

☐ Results verified the lack of relevant prior art (helped determine patentability).

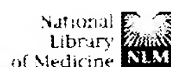
☐ Search results were not useful in determining patentability or understanding the invention.

Other Comments:

Drop off completed forms at the Circulation Desk CM-1, or send to Mary Hale, CM-1E01 or e-mail [mary.hale@uspto.gov](mailto:mary.hale@uspto.gov).







PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

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1: J Interferon Cytokine Res 2000 Dec;20(12):1057-63

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## Modulation of IgE response and cytokine production in Peyer's patches and draining lymph nodes in sensitized mice made tolerant by oral dust mite administration.

Maciel M, Fusaro AE, Duarte AJ, Sato MN.

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Services

Laboratorio de Alergia e Imunologia Clínica e Experimental/LIM-56, Faculdade de Medicina da Universidade de São Paulo-Brasil.

Related  
Resources

Such allergic diseases as rhinitis and asthma are IgE-mediated type I reactions and are controlled primarily by Th2 cells. One of the major dust mites, *Dermatophagoides pteronyssinus* (Dp), is considered to cause allergic reactions. Oral tolerance, largely used to modulate immune response, opens the possibility of modulating Th2 allergic responses. We observed downmodulation of total and specific IgE antibody levels as well as the number of specific IgE-secreting cells with Dp feeding in previously sensitized mice. Analysis of the cytokine profile in mucosal lymphoid tissues in the protocol revealed altered patterns of interferon-gamma (IFN-gamma), interleukin-5 (IL-5), and transforming growth factor-beta (TGF-beta) secretion in Dp-fed animals. The results suggest that both the Th and B cell populations are modulated in mice made tolerant by oral Dp feeding. Understanding the mechanisms at the mucosal level that underlie oral tolerance can improve its use in allergy immunotherapy.

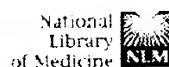
PMID: 11152571 [PubMed - indexed for MEDLINE]

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1: Experientia 1991 Sep 15;47(9):905-12

Related Articles, Links

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## Production of pharmaceutical proteins in milk.

Wilmut I, Archibald AL, McClenaghan M, Simons JP, Whitelaw CB, Clark AJ.

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AFRC Institute of Animal Physiology and Genetics Research, Roslin, Midlothian, Scotland.

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There is every reason to expect that it will be possible within the next few years to begin to use farm animals to produce large quantities of some of the human proteins that are needed for the treatment of disease. Revolutionary new opportunities for the production of novel proteins in milk have been created by the development of methods for gene transfer. Exploitation of these opportunities depends upon selection and cloning of milk protein genes and identification of the sequences that govern tissue specific hormonally induced expression in the mammary gland. Studies with three genes, ovine beta-lactoglobulin, rat beta-casein and whey acidic protein of rat and mouse, suggest that they may all meet this requirement. Fragments of the ovine beta-lactoglobulin, murine whey acidic protein and rabbit beta-casein genes have directed production of novel proteins in the milk of transgenic mice, sheep, rabbits and pigs. The proteins were biologically active and usually co-migrated with authentic proteins. In early experiments, protein concentration was low, but our recent observations suggest that fusion genes containing genomic clones direct production of concentrations of protein that are suitable for commercial exploitation. In the longer term, two approaches may offer the potential of more reliable expression. Control elements capable of directing expression that is independent of site of insertion of the gene, but dependent on the number of copies of the gene, have been identified for a small number of genes. The availability of such elements for the milk protein genes would increase the reliability of gene expression considerably. Alternatively, targeted mutation of genes may allow the insertion of coding sequences within an existing gene so avoiding position effects.

### Publication Types

- Review
- Review, Tutorial

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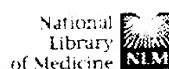
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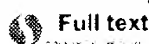
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**Oral tolerance induced to house dust mite extract in naive and sensitized mice: evaluation of immunoglobulin G anti-immunoglobulin E autoantibodies and IgG-IgE complexes.**

**Sato MN, Carvalho AF, Silva AO, Maciel M Jr, Fusaro AE, Duarte AJ.**

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Laboratorio de Imunogenetica e Transplante Experimental LIM-56, Faculdade de Medicina da USP (FMUSP), Sao Paulo, Brasil.

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We investigated the effect on specific antibody response of naive and sensitized mice orally administrated with low (0.25 mg) or high (10.0 mg) doses of *Dermatophagoides pteronyssinus* (Dp) extract. We also examined the effect of oral administration of Dp on the production of autoantibodies to immunoglobulin G (IgG) and immunoglobulin E (IgE). Naive and sensitized mice both showed a marked down-regulation of IgE antibody production, regardless of the dose of Dp. We also detected an inhibitory effect of the total IgE levels and the allergen-specific IgG1, IgG2a and IgG2b antibody response in sensitized mice given the low dose of Dp. In contrast, high doses of Dp stimulated IgG1 antibody production in both naive and sensitized animals. In addition, the oral tolerance induction protocol stimulated anti-F(ab')<sub>2</sub>gamma and anti-Fcgamma autoantibody production. Evaluation of IgG anti-IgE autoantibodies by a direct enzyme immunoassay (EIA) revealed the presence of these autoantibodies, predominantly of the IgG1 isotype, specifically in those animals fed with the high dose. In contrast, IgG-IgE complexes, determined by EIA using immobilized anti-IgE antibodies, were detected mainly in sera of control animals. The autoantibody anti-IgE specificity was tested against IgE-TNP and IgE-DANSYL murine proteins and revealed different inhibition profiles, suggesting the action of heterogeneous subpopulations of autoantibodies. Taken together, our results show that the oral tolerance protocol with Dp was able to modulate the production of allergen-specific IgE antibodies in both naive and sensitized animals. In addition, we suggest that anti-IgE autoantibodies participate in the modulation of allergic response triggered by oral tolerance protocols.

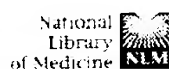
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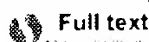
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1: Immunology 1999 Nov;98(3):338-44

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**Low dose of orally administered antigen down-regulates the T helper type 2-response in a murine model of dust mite hypersensitivity.**

Sato MN, Carvalho AF, Silva AO, Maciel M Jr, Fusaro AE, Duarte AJ.

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Laboratorio de Alergia e Imunologia Clinica e Experimental-LIM 56, Faculdade de Medicina da Universidade de Sao Paulo, Sao Paulo, Brazil.

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One of the main goals of immunotherapy of allergic diseases is the down-regulation of the type I hypersensitivity reaction. We investigated in this study the effect of oral administration of varying doses (0.25, 1.0, 4.0 and 10 mg) of dust mite extract (*Dermatophagoides pteronyssinus*, Dp) in sensitized A/Sn mice. A marked decrease of the allergen-specific immunoglobulin E (IgE) response was observed with all antigen doses. The mice orally tolerized with low Dp dose (0.25 mg) had a significant decrease in the total serum IgE and in the immunoglobulin G1 (IgG1), IgG2a and IgG2b antibody levels. The higher Dp dose (10.0 mg), however, enhanced the IgG1 antibody response, suggesting the stimulation of a pre-existing immune response of the sensitized animals. Animals fed with the low Dp dose had a significant decrease in the frequency of interleukin-4 (IL-4) secreting cells. These animals also showed a significant decrease in the frequency of Dp-specific IgE- and IgG1-positive plasma cells. Our data suggest that feeding dust mite extract to Dp-sensitized mice down-regulates the development of type I hypersensitivity, by inhibition of the T helper 2 response.

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